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DR PROST1; PS00031; NUCLEAR RECEPTOR; 1.
 KW DNA-binding; Metal-bind.; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; zinc-finger.
 SQ SEQUENCE 896 AA; 97094 MW; 440F5P6E73BC796 CRC64;

Query Match 98.4%; Score 1349.5; DB 6; Length 896;
 Best Local Similarity 99.6%; Pred. No. 3 5e-119; Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 65 SH-IRGYEYEQPIFLVNLRAIBPGVCAAGHNNQDPSAALLSSNELGERQLVHVVKWK 713
 Qy 62 ALPGFRNTLHDQMAVIOQSWMGLNVFANGWRSFTNVSNSRMLYFAPDLVNEVTRMKSRM 121
 Db 714 ALPGFRNTLHDQMAVIOQSWMGLNVFANGWRSFTNVSNSRMLYFAPDLVNEVTRMKSRM 773

Qy 2 SHMIGEYECOPFLVNLRAIBPGVCAAGHNNQDPSAALLSSNELGERQLVHVVKWK 61
 Db 639 SH-IRGYEYECOPFLVNLRAIBPGVCAAGHNNQDPSAALLSSNELGERQLVHVVKWK 697

Qy 62 ALPGFRNLHDQMAVIOQSWMGLNVFANGWRSFTNVSNSRMLYFAPDLVNEVTRMKSRM 121
 Db 698 ALPGFRNLHDQMAVIOQSWMGLNVFANGWRSFTNVSNSRMLYFAPDLVNEVTRMKSRM 757

Qy 122 YSQCVRMHLISQEFGMLOITPQEFCLMKALLSIIIPVGLKNOKEFDLMNYIKELR 181
 Db 758 YSQCVRMHLISQEFGMLOITPQEFCLMKALLSIIIPVGLKNOKEFDLMNYIKELR 817

Qy 182 IIACKRKNPITSCSRFPYFHTQ 241
 Db 818 IIACKRKNPITSCSRFPYFHTQ 877

Qy 242 VQVPKILSGKVPKPYFHTQ 260
 Db 878 VQVPKILSGKVPKPYFHTQ 896

RESULT 2

Q8MIKO PRELIMINARY; PRT; 912 AA.

ID Q8MIKO; PRELIMINARY; PRT; 912 AA.

AC Q8MIKO; PRELIMINARY; PRT; 912 AA.

DT 01-OCT-2002 (TREMBREL. 22, Created)

DT 01-OCT-2002 (TREMBREL. 22, Last annotation update)

PT 01-MAR-2003 (TREMBREL. 23, Last annotation update)

DE Androgen receptor.

OS Crocuta crocata. (Spotted hyena).

OC Mammalia; Buteraria; Carnivora; Fissipedia; Hyenidae; Crocata.

OX NCBI_TaxID:9678;

RN 11
 SEQUENCE FROM N.A.

RA Catalano S., Avila D.M., McPhaul M.J., Marsico S., Wilson J.D.,
 RA Glickman S.E.;

RT "Absence of association of the virilization of the female spotted hyena with alterations of the amino acid sequence of the androgen receptor (Ar)." ;

RL Mol. Cell. Endocrinol. 0:0-0(2002).
 CC -- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

RT receptor (Ar);

DR IPRO01103; Androgen receptor.

DR IPRO011628; Znf C4steroid.

DR IPRO0056; Hormone rec. lig.

DR IPRO0056; Hormone rec. lig.

DR IPRO01628; Znf C4steroid.

DR PFAM; PF01166; Androgen receptor; 1.

DR EMBL; ARN62704; AD45921.1; -.

DR HSSP; P06536; IGDC.

DR InterPro; IPRO01103; Androgen receptor.

DR InterPro; IPRO0056; Hormone rec. lig.

DR InterPro; IPRO01628; Znf C4steroid.

DR PFAM; PF01104; hormone_rec; 1.

DR PFAM; PF00105; zf-C4; 1.

DR PRINTS; PR00047; STROUDINGER.

DR PRODOM; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HolI; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROST1; PS00031; NUCLEAR RECEPTOR; 1.

DR PROST1; PS00031; NUCLEAR RECEPTOR; 1.

DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

KW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 912 AA; 99557 MW; 8F5EC5B1E43C51 CRC64;

Query Match 97.5%; Score 1336.5; DB 4; Length 906;
 Best Local Similarity 98.5%; Pred. No. 6e-118; Matches 255; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 708 SH-IRGYEYECOPFLVNLRAIBPGVCAAGHNNQDPSAALLSSNELGERQLVHVVKWK 61
 Qy 62 ALPGFRNLHDQMAVIOQSWMGLNVFANGWRSFTNVSNSRMLYFAPDLVNEVTRMKSRM 767

Db 649 SH-IRGYEYECOPFLVNLRAIBPGVCAAGHNNQDPSAALLSSNELGERQLVHVVKWK 707

Qy 122 YSQCVRMHLISQEFGMLOITPQEFCLMKALLSIIIPVGLKNOKEFDLMNYIKELR 181
 Db 768 YSQCVRMHLISQEFGMLOITPQEFCLMKALLSIIIPVGLKNOKEFDLMNYIKELR 827

OS DB
Androgen receptor (Fragment).
Poecilia guttata (Zebra Finch) (*Taeniopygia guttata*)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosaura; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
NCBI_TaxID=59729;
[1] -
SEQUENCE FROM N.A.
Perlman W.R., Ramachandran B., Arnold A.P.;
"Expression of Androgen Receptor mRNA in the Late Embryonic and Early Post-hatch Zebra Finch Brain.",
Submitted (TURL-2002) to the EMBL/GenBank/DBJ databases.
- - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC : BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
EMBL: AF533914; AAC96599.1; -.
InterPro: IPR005536; Hormone_rec_lig.
InterPro: IPR01628; Znf_C4steroid_receptor.
InterPro: IPR01628; Znf_C4steroid.
Pfam: PF00104; hormone_rec_1.
PFAM: PF00105; zf-C4; 1.
PRINTS: PR00398; STRDIORMONER.
PRODOM: PD000035; Znf_C4steroid; 1.
SMART: SM00430; HOLL_1.
SM00399; Znf_C4; 1.
KW DNA-binding; Metal-Binding; Nuclear protein; Receptor; Transcription; RNA transcription regulation; Zinc; Zinc-finger.
NON_TER 1
FT SEQQUENCE 333 AA; 38536 MW; B36A778B710B790 CRC64;
Query Match 93.7%; Score 1285; DB 13; Length 333;
Best Local Similarity 93.4%; Pred. No. 1.4e-113;
Matches 239; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
Oy 5 ISGYRCQIPINLATEIPGVVCAHHNQNPDSPAALISSNLGEROLVHVKWAQLP 64
Db 78 IDGQECQIPFLNLTAREPGVVCAHHNQNPDSPAALISSNLGEROLVYVVKWAKLP 137
Oy 65 GFRNLHDQDMAVIOYSQNGLMTPAMGRSPFNNRSMYFADLVNRYMRKRSMSQ 124
Db 138 GRNLHDQDMASIQYSQNGLMTPAMGRSPFNNRSMYFADLVNRYMRKRSMSQ 197
Oy 125 CYTRRHISQFGMQLTTQEPFLKALLFLSIPVGDKKNQKFDELUNNYKELDRITA 184
Db 198 CIRNRHISQFGMQLTTQEPFLKALLFLSIPVGDKKNQKFDELUNNYKELDRITA 257
Oy 185 CRRKPNPSCSRRYQTLKLDSQPIARLHQPTDILKSHNSVDPPEMMARIISQV 244
Db 258 CRRKPNPSCSRRYQTLKLDSQPIARLHQPTDILKSHNSVDPPEMMARIISQV 317
Oy 245 PKLSSGKPKIYHQA 260
Db 318 PKLSSGKPKIYHQA 333
RESULT 7
P70048
ID P70048 PRELIMINARY; PRT; 790 AA.
DT 01-FEB-1997 (TREMBrel. 02, Created)
DT 01-JAN-1999 (TREMBrel. 09, Last sequence update)
DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)
GN Alpha_AR
DE Androgen receptor alpha isoform.
OS Xenopus laevis (African clawed frog).
OC Xanthopis laevis (African clawed frog).
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopoda; Xenopus.
OX NCBI_TaxID=8335;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=93376782; PubMed=7690145;
RA Fischer L.J.; Catz D.; Kelley D.;
RA "An androgen receptor mRNA isoform associated with hormone-induced
cell proliferation." Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258 (1993).
RL RPL
RN [2] SEQUENCE FROM N.A.
RN RPL
RP SEQUENCE FROM N.A.
RN RPL
RX MEDLINE=95524753; PubMed=7601302;
RA Fischer L.M.; Catz D.; Kelley D.B.;
RT "Androgen-directed development of the *Xenopus laevis* larynx: control
of androgen receptor expression and tissue differentiation." Biol. 170:115-126 (1995).
RL RPL
RN [3] SEQUENCE FROM N.A.
RA Kelley D.B.; Kamenetz F.R.; Kelley D.B.; Badea T.C.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL: U67129; AAC97386.1; -.
DR RPPS; P06556; IGDC.
InterPro: IPR001103; Androgen receptor.
Pfam: PF00104; hormone_rec_1.
PRINTS: PR00047; STRDIORMONER.
PRODOM: PD000035; Znf_C4steroid; 1.
SMART: SM00430; HOLL_1.
SM00399; Znf_C4; 1.
KW DNA-binding; Metal-Binding; Nuclear protein; Receptor; Transcription; RNA transcription regulation; Zinc; Zinc-finger.
NON_TER 1
FT SEQQUENCE 790 AA; 86973 MW; 9E7FC136CCCC906 CRC64;
Query Match 89.3%; Score 1224; DB 13; Length 790;
Best Local Similarity 88.4%; Pred. No. 2.4e-107;
Matches 228; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
Oy 1 GSHMIGKCYCQIPINLATEIPGVVCAHHNQNPDSPAALISSNLGEROLVHVKWA 60
Db 531 GIPOLBGYSCQIPFLNLTAREPGVVCAHHNQNPDSPAALISSNLGEROLVYVVKWA 590
Oy 61 KALPGEFNLHDQDMAVIOYSQNGLMTPAMGRSPFNNRSMYFADLVNRYMRKSR 120
Db 591 KALPGEFNLHDQDMAVIOYSQNGLMTPAMGRSPFNNRSMYFADLVNRYMRKSR 650
Oy 121 MYSQCYTRRHISQFGMQLTTQEPFLKALLFLSIPVGDKKNQKFDELUNNYKELDRITA 180
Db 651 MYSQCYTRRHISQFGMQLTTQEPFLKALLFLSIPVGDKKNQKFDELUNNYKELDRITA 710
Oy 181 RIACKRKNPSCSRRYQTLKLDSQPIARLHQPTDILKSHNSVDPPEMMARIISQV 240
Db 711 RIVSKRKNPSCSRRYQTLKLDSQPIARLHQPTDILKSHNSVDPPEMMARIISQV 770
Oy 241 SVQVPKILSGKPKIYHQA 258
Db 771 SVQVPKILSGKPKIYHQA 788
RESULT 8
ID O91445 PRELIMINARY; PRT; 344 AA.
ID O91445 PRELIMINARY; PRT; 344 AA.
AC O91445;
DT 01-NOV-1995 (TREMBrel. 01, Created)
DT 01-NOV-1995 (TREMBrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)
DE Androgen receptor (Fragment).
GN AR.
OS Serinus canaria (Canary).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Archosaura; Aves; Neognathae; Passeriformes; Passeroidea;
OC Fringillidae; Carduelinae; Serinus.
OX NCBI_TaxID=9135;
RP SEQUENCE FROM N.A.

DR SMART; SMO0430; HOLL; 1.
 DR SMART; SMO139; Znf C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW Transcription; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW SEQUENCE 853 AA; 95776 MW; 6SEFF5FD336F4C4 CRC64;

Query Match 68.2%; Score 935; DB 13; Length 853;
 Best Local Similarity 70.4%; Pred. No. 6. 6e-80;
 Matches 178; Conservative 35; Mismatches 36; Indels 4; Gaps 2;

Qy 8 YECQPFLNVLLEIEPGVVCAGHNNQDPSFAALLSLNELLGEROLVHVVKAKLPGF 67
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db FHSQILFLNLTELESPEPVNAGHAQPSAVALTSINELGEROLVHVVKAKLPGF 647

Qy 68 NLHVDDOMAVIYQSYWGLMVFAMGWSRFNTNSRMLYFAPDLYPNEVYRMHKSRSYQCTR 127
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db NLHVDDOMTVIYQSYWGLMVFAMGWSRFNTNSRMLYFAPDLYPNEVYRMHKSRSYQCTR 707

Qy 602 FHSQQLVNLTELESPEPVNAGHAQPSAVALTSINELGEROLVHVVKAKLPGF 67
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db MRHLISQBPGLQITPQRPLCMKALLFSIIPVNGAKSOKYFDBRLRYTINELDRVINYGR 661

Qy 68 NLHVDDOMAVIYQSYWGLMVFAMGWSRFNTNSRMLYFAPDLYPNEVYRMHKSRSYQCTR 127
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db MKHLISQBPVLQVNTPEFLCMKALLFSIIPVNGAKSOKYFDBRLRYTINELDRVINYGR 767

Qy 662 NLHVDDOMTVIYQSYWGLMVFAMGWSRFNTNSRMLYFAPDLYPNEVYRMHKSRSYQCTR 721
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db KNPTSCRRPYTQLDSDVOPAHLHQFTFLIKSMV-SUDPFEMMAELISVQWP 245
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 782 K-SNCSPRPYQTLRMDLSQPIVRKLQOPTDFLPIQASLPTKVSPPMELISVQWP 839
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 246 KILSGKVKEPYFH 258
 : |||:|||:
 Db 840 KILAGLAXPILFH 852
 : |||:|||:
 Db 826 KILAGLSKLPILFH 838
 : |||:|||:

RESULT 11

ID 08QFV2 PRELIMINARY; PRT; 839 AA.

ID 08QFV2 PRELIMINARY; PRT; 839 AA.

AC 08QFV2; PRELIMINARY; PRT; 839 AA.

PT 01-JUN-2002 (TREMBREL. 21, Created)
 DT 01-MAR-2003 (TREMBREL. 23, Last sequence update)

DE Androgen receptor.

GN AR.

OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OC NCBI_TaxID=7957;
 RN [1]

RP TISSUE-LIVER.

RC Betka M., Rothberg S.C., Callard G.V.,
 RT "Carassius auratus Androgen Receptor";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

DR EMBL; AX0397; AM09278.1; -.

DR InterPro; IPR001103; Andrgn receptor.

DR InterPro; IPR000536; Hormone_rec_lig.

DR InterPro; IPR00536; Hormone_rec_lig.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF02166; Androgen_Recep; 1.

DR Pfam; PF00104; hormone_rec; 1.

DR Pfam; PF00104; hormone_rec; 1.

DR Pfam; PF00105; zf-C4; 1.

DR Prodrom; PD000035; Znf_C4steroid; 1.

DR SMART; SMO0430; HOLL; 1.

DR SMART; SMO0399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription; Zinc; Zinc-finger.

SEQUENCE 839 AA; 93168 MW; A534D3169C0B1PA CRC64;

Qy 8 YECQPFLNVLLEIEPGVVCAGHNNQDPSFAALLSLNELLGEROLVHVVKAKLPGF 67
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db FHSQILFLNLTELESPEPVNAGHAQPSAVALTSINELGEROLVHVVKAKLPGF 647

Query Match 67.7%; Score 928; DB 13; Length 769;
 Best Local Similarity 70.8%; Pred. No. 2. 7e-79;
 Matches 179; Conservative 29; Mismatches 41; Indels 4; Gaps 2;

Qy 8 YECQPFLNVLLEIEPGVVCAGHNNQDPSFAALLSLNELLGEROLVHVVKAKLPGF 67
 : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 516 FNSQVFLNVLLESIREPVNAGHGYQPSAATLTSNLGEQLVKVKWAKLPGF 577

Query Match 67.8%; Score 930; DB 13; Length 839;
 Best Local Similarity 70.4%; Pred. No. 1. 9e-79;
 Matches 178; Conservative 35; Mismatches 36; Indels 4; Gaps 2;

Db 578 NLVYDDQMVIVLQHISWGMVNVFGLGWRSYKVNNSRLYFAPDLVNEHRHMHSITMHCIR 637 Qy 188 KNPTSCSRPFVQLTKLSDVPIARELHQFTFDLILKSHM--SVDPPEMMARISVQVP 245
 Qy 128 MRHLSQBEGWLOQTPOETCMKALLFSTIPVOCILKQKPFELRMVYKEDRILACKR 187 Db 638 MRHLSQBFLQIOTOBECMKALLFSIPVEGLKSQKFDELRLTYINELDRLLINRM 697
 Db 188 KNPTSCSRPFVQLTKLSDVPIARELHQFTFDLILKSHM--SVDPPEMMARISVQVP 245
 Qy 698 N--TNCSDRFYQFLTRILDSLQMTVKKLUHFTDFLVQASLPTKVSPMEMCIRISVHP 755
 Qy 246 KILSGKVVKPIYFH 258
 Db 756 KULAGLAKPILFH 768
 RESULT 13
 ID Q9PWGS PRELIMINARY; PRT; 797 AA.
 ID Q9PWGS PRELIMINARY; PRT; 797 AA.
 AC Q9PWGS;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)
 DB Androgen receptor-beta.
 GN AR-BETA.
 OS Anguilla japonica (Japanese eel).
 OC Bokaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OX NCBI_TaxID=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=99195076; PubMed=10464240;
 RA IKeuchi T.; Todo T.; Kobayashi T.; Nagahama Y.;
 RT "cDNA cloning of a novel androgen receptor subtype.";
 RL J. Biol. Chem. 274:22205-22205(1999).
 CC -- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR -- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 EMBL: AB025361; BRA8805.1; --.
 DR HSSP; P06556; IGD;
 DR InterPro; IPR001103; Androgen receptor.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Sterbmun receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR PFam; PF0166; Androgen_Recep; 1.
 DR PFam; PF000104; hormone_rec; 1.
 DR PFam; PF000105; zf-C4; 1.
 DR PRINTS; PR00398; STRDORMONER.
 DR PRINTS; PR00047; STRDOPINGER.
 DR SMART; SM00430; HOMI; 1.
 DR SMART; SM00395; Znf_C4steroid.
 DR PROSITE; PS00031; NUCLEAR_RECPRTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 563 AA; 64352 MW; A744C3728F004AF6 CRC64;
 Query Match 67.5%; Score 925; DB 13; Length 797;
 Best Local Similarity 69.2%; Pred. No. 5; 4e-79;
 Matches 175; Conservative 35; Mismatches 39; Indels 4; Gaps 2;
 Qy 8 YECQPIPLAVLAEIPEGVCAHHDNQPSFAAIISSLNELGERQVHVVKAKLPGFR 67
 Db 546 FPTQSPLNLTIESPEPVVNGHDXGQTDAAATLJLHSNLGERQFLVKVWKALPGFR 605
 Qy 68 NLVYDDQMVIVLQHISWGMVNVFGLGWRSYKVNNSRLYFAPDLVNEHRHMHSITMHCIR 127
 Db 606 NMVHDQDMVIVLQHISWGMVNVFGLGWRSYKVNNSRLYFAPDLVNEHRHMHSITMHCIR 431
 Qy 188 KNPTSCSRPFVQLTKLSDVPIARELHQFTFDLILKSHM--SVDPPEMMARISVQVP 245
 Db 492 K--TNCSDRFYQFLTRILDSLQMTVKKLUHFTDFLVQASLPTKVSPMEMCIRISVHP 549
 Db 666 MRHLSQBFLQIOTOBECMKALLFSIPVEGLKSQKFDELRLTYINELDRLLINRM 725
 Qy 246 KILSGKVVKPIYFH 258
 RESULT 14
 ID Q9DDJ4 PRELIMINARY; PRT; 563 AA.
 AC Q9DDJ4;
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DB Androgen receptor (Fragment).
 GN AR.
 OS Halichoeres trimaculatus (Three-spot wrasse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleoste; Neoteleoste;
 OC Acanthomorpha; Acanthopterygii; Perciforma; Perciformes; Labroidei;
 OC Labridae; Halichoeridae.
 RN NCBI_TaxID=147232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim S.-J.; Kei O.; Takemura A.; Nakamura M.;
 RT Partial sequence and expression of androgen and estrogen receptor genes in the protogynous wrasse, Halichoeres trimaculatus.";
 RL Submitted (DEG-2000) to the EMBL/GenBank/DDBJ databases.
 CC -- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AR26200; AA648340.1; --.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Sterbmun receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR PFam; PF00104; hormone_rec; 1.
 DR PRINTS; PR00398; STRDORMONER.
 DR PRINTS; PR00047; STRDOPINGER.
 DR SMART; SM00430; HOMI; 1.
 DR SMART; SM00395; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECPRTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT NON_TER 1 1
 SQ SEQUENCE 563 AA; 64352 MW; A744C3728F004AF6 CRC64;
 Query Match 66.4%; Score 911; DB 13; Length 563;
 Best Local Similarity 69.6%; Pred. No. 7; 5e-78;
 Matches 176; Conservative 31; Mismatches 42; Indels 4; Gaps 2;
 Qy 8 YECQPIPLAVLAEIPEGVCAHHDNQPSFAAIISSLNELGERQVHVVKAKLPGFR 67
 Db 312 FPTQSPLNLTIESPEPVVNGHDXGQTDAAATLJLHSNLGERQFLVKVWKALPGFR 371
 Qy 68 NLVYDDQMVIVLQHISWGMVNVFGLGWRSYKVNNSRLYFAPDLVNEHRHMHSITMHCIR 127
 Db 372 NLVYDDQMVIVLQHISWGMVNVFGLGWRSYKVNNSRLYFAPDLVNEHRHMHSITMHCIR 431
 Qy 128 MRHLSQBEGWLOQTPOETCMKALLFSTIPVOCILKQKPFELRMVYKEDRILACKR 187
 Db 432 MRHLSQBFLQIOTOBECMKALLFSIPVEGLKSQKFDELRLTYINELDRLLINRM 491
 Qy 188 KNPTSCSRPFVQLTKLSDVPIARELHQFTFDLILKSHM--SVDPPEMMARISVQVP 245
 Db 492 K--TNCSDRFYQFLTRILDSLQMTVKKLUHFTDFLVQASLPTKVSPMEMCIRISVHP 549
 Qy 246 KILSGKVVKPIYFH 258

Search completed: October 9, 2003, 11:42:15
Job time : 39 SECS

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OM protein - protein search, using sw model

Run on:

Perfect score: 1371

Sequence: US-09-687-609A-1

US-09-687-609A-1
1 GSHMIEGECQPIFLNVEA..... SVQVPKILSGKVPIYFHTQ 260

Title: US-09-687-609A-1
Search time 11 Seconds
(without alignments)
111.540 Million cell updates/sec

Scoring table:

BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched:

12863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1349.5	98.4	709	1 ANDR_RABIT	P49699 oryctolagus cuniculus (Rabbit);
2	1349.5	98.4	884	1 ANDR_EULFC	097776 eulemur fulvus (Ring-tailed lemur);
3	1349.5	98.4	891	1 ANDR_MACFA	097960 papio hamadryas (Chacma baboon);
4	1349.5	98.4	895	1 ANDR_PAPHA	097961 mus musculus (House mouse);
5	1349.5	98.4	899	1 ANDR_MOUSE	P19031 mus musculus (House mouse);
6	1349.5	98.4	902	1 ANDR_RAT	P15207 rattus norvegicus (Norway rat);
7	1349.5	98.4	907	1 ANDR_CANFA	Q9T800 canis familiaris (Domestic dog);
8	1349.5	98.4	911	1 ANDR_PANTR	097775 pan troglodytes (Orangutan);
9	1349.5	98.4	919	1 ANDR_HUMAN	097275 homo sapiens (Human);
10	766	55.9	930	1 PRGR_RABIT	P06386 oryctolagus cuniculus (Rabbit);
11	765	55.8	933	1 PRGR_HUMAN	P06401 homo sapiens (Human);
12	759	55.4	923	1 PRGR_RAT	Q63449 rattus norvegicus (Norway rat);
13	758	55.3	923	1 PRGR_MOUSE	Q00175 mus musculus (House mouse);
14	752	54.9	786	1 PRGR_CHICK	P07812 gallus gallus (Domestic fowl);
15	738	53.8	377	1 PRGR_SHEEP	Q28590 ovis aries (Sheep);
16	677.5	49.4	359	1 MCR_ONCNY	Q9i466 oncorhynchus tshawytscha (Salmon);
17	666	48.6	978	1 MCR_MOUSE	Q8VX18 mus musculus (House mouse);
18	665	48.5	984	1 MCR_HUMAN	P08235 homo sapiens (Human);
19	664.5	48.5	777	1 GCR_ACTINA	P79886 actinia nancyae (Actinia);
20	664.5	48.5	777	1 GCR_SALBB	O13186 salmire bolei (Salmire);
21	664.5	48.5	778	1 GCR_SALISC	P04567 salmire sciatica (Salmire);
22	662.5	48.3	777	1 GCR_HUMAN	P04150 homo sapiens (Human);
23	662	48.3	981	1 MCR_RAT	P22199 rattus norvegicus (Norway rat);
24	662	48.3	1 MCR_SALISC	P08078 salmire sciatica (Salmire);	
25	661.5	48.2	777	1 GCR_SAGOE	P79269 sagomia oe (Sagomia);
26	660.5	48.2	772	1 GCR_RABITA	P59667 orcytolagus cuniculus (Rabbit);
27	660	48.1	612	1 MCR_XENLA	Q91773 xenopus laevis (African clawed frog);
28	657.5	48.0	783	1 GCR_MOUSE	P06537 mus musculus (House mouse);
29	652.5	47.6	776	1 GCR_TUGFB	Q95267 tupaias glis (Tupaias);
30	651.5	47.5	807	1 GCR_PAROL	Q73673 paralichthys olivaceus (Olive flounder);
31	650.5	47.4	776	1 GCR_XENLA	P49944 xenopus laevis (African clawed frog);
32	648.5	47.3	758	1 GCR_ONCNY	P49843 oncorhynchus tshawytscha (Salmon);
33	644.5	47.0	771	1 GCR_CAVPO	P49115 cavia porcellus (Guinea pig);

ALIGNMENTS

34	639.5	46.6	795	1 GCR_RABIT	P06535 rattus norvegicus (Norway rat);
35	615	44.9	977	1 MCR_TUPGB	Q29331 tupaias glis (Tupaias);
36	590	43.0	258	1 MCR_SHBEP	Q91617 ovis aries (Sheep);
37	580	42.3	711	1 GCR_PIG	P79404 sus scrofa (Pig);
38	391	28.5	164	1 MCR_PIG	P73373 macroscelides proboscideus (Aardvark);
39	387	28.2	180	1 PRGR_MACBU	Q8ph12 gallus gallus (Domestic fowl);
40	342	24.9	147	1 MCR_CHICK	P57717 brachyramphus hypoleucus (Brachyramphus);
41	237	17.3	569	1 ESRI_BRARE	Q42132 pagrus major (Sea bream);
42	228.5	16.7	581	1 ESRI_PAGMA	Q91727 icthalius punctatus (Paganella);
43	227.5	16.6	617	1 ESRI_ICIPU	Q91424 cnemidophorus lateralis (Lizard);
44	223	16.3	307	1 ESRI_CNEUN	P50242 salmo salar (Salmon);
45	222	16.2	535	1 ESRI_SALSA	

PT	ZN_FING	349	369	C4-TYPE.	DR	TRANSFAC; T04655; -.
PT	ZN_FING	385	409	C4-TYPE.	DR	InterPro; IPR01133; Andrgn receptor.
PT	DOMAIN	480	709	LIGAND-BINDING.	DR	InterPro; IPR00056; Hormone_rec_lig.
PT	DOMAIN	3	6	POLY-GLN.	DR	InterPro; IPR01733; Sidhrm receptor.
PT	DOMAIN	182	187	POLY-PRO.	DR	InterPro; IPR01628; znt Castroid.
PT	DOMAIN	201	207	POLY-ALA.	DR	Pfam; PRO2166; Androgen_Recpt; 1.
PT	SEQUENCE	254	262	POLY-GLY.	DR	Pfam; PR00104; hormone_rec; 1.
SQ	709 AA;	77391 MW;	408766137E97B6B	CRC64;	DR	PRINTS; PR0047; STRDHORMONER.
Query Match	98.4%;	Score 1349.5;	DB 1;	Length 709;	DR	PRINTS; PR00035; Znf_C4steroid; 1.
Best Local Similarity	99.6%;	Pred. No. 2.4e-118;	0;	Mismatches 0;	DR	SMART; SM00430; Holi; 1.
Matches 258;	Conservative	1;	Indels 1;	Gaps 1;	DR	SMART; SM00393; Znf_C4; 1.
Qy	2 SHMIEGYCQPIFLVNLRAIEPGVCAGHDDNNQDPSFAALLSSLNELGEROLHVVKWAK	61	61	DR	PROSITE; PS00031; NUCLEAR RECEPTOR; 1.	
Db	452 SH-IEGYECQPIFLVNLRAIEPGVCAGHDDNNQDPSFAALLSSLNELGEROLHVVKWAK	510	510	KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein;	
Qy	62 ALPGERNLHVDDOMAVIOVQSYNGMLVAMGWSRFTNNSRMLYFADPLVENEYRMKSRM	121	121	KW	Zinc-finger; Steroid-binding; MODULATING (BY SIMILARITY).	
Db	511 ALPGERNLHVDDOMAVIOVQSYNGMLVAMGWSRFTNNSRMLYFADPLVENEYRMKSRM	570	570	FT	DNA_BIND 524 589 NUCLEAR RECEPTOR-TYPE.	
Qy	122 YSQCVVRNLHSQERGMQLQTPOFLCMKALIISIIPVGDKNQKFDELARMYKELDR	181	181	FT	ZN_FING 524 544 C4-TYPE.	
Db	571 YSQCVVRNLHSQERGMQLQTPOFLCMKALIISIIPVGDKNQKFDELARMYKELDR	630	630	FT	ZN_FING 560 584 C4-TYPE.	
Qy	182 IIACKRKNTCSRSRFYVOLTKLDSVOPARELHOFTDLIKSHMVSDFPEMMARIS	241	241	FT	DOMAIN 55 884 LIGAND-BINDING.	
Db	631 IIACKRKNTCSRSRFYVOLTKLDSVOPARELHOFTDLIKSHMVSDFPEMMARIS	690	690	FT	DOMAIN 64 70 POLY-GLN.	
Qy	242 VQVKLISKGVKPKIYFHTQ 260	260	260	FT	DOMAIN 116 120 POLY-ALA.	
Db	691 VQVKLISKGVKPKIYFHTQ 709	709	709	FT	DOMAIN 174 178 POLY-GLN.	
RESULT 2	ANDR_EULFC	STANDARD;	PRT;	884 AA.	FT	DOMAIN 353 362 POLY-PRO.
ID	ANDR_EULFC	STANDARD;	PRT;	884 AA.	FT	DOMAIN 379 383 POLY-ALA.
AC	097776;				FT	DOMAIN 408 411 POLY-ALA.
DT	30-MAY-2000 (Rel. 39; Last sequence update)				FT	DOMAIN 430 435 POLY-GLY.
DT	30-MAY-2000 (Rel. 39; Last annotation update)				SQ	SEQUENCE 884 AA; 9510 MW; 18P57BB352F4D2BD CRC64;
DE	Androgen receptor (Dihydrotestosterone receptor).				Query Match	98.4%; Score 1349.5; DB 1; length 884;
GN	NR_00347.				Best Local Similarity	99.6%; Pred. No. 3.1e-118; 0; Mismatches 0; Indels 1; Gaps 1;
BR	Bulemur fulvus collaris (Colored brown lemur).				Matches 258;	Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OS	Bulemur; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Qy	2 SHMIEGYCQPIFLVNLRAIEPGVCAGHDDNNQDPSFAALLSSLNELGEROLHVVKWAK
OC	Mammalia; Buteraria; Primates; Strepsirrhini; Lemuridae; Bulemur.				Db	627 SH-IEGYECQPIFLVNLRAIEPGVCAGHDDNNQDPSFAALLSSLNELGEROLHVVKWAK
OX	NCBI_TaxID=47178;				Qy	62 ALPGERNLHVDDOMAVIOVQSYNGMLVAMGWSRFTNNSRMLYFADPLVENEYRMKSRM
RN	[1]				Db	686 ALPGERNLHVDDOMAVIOVQSYNGMLVAMGWSRFTNNSRMLYFADPLVENEYRMKSRM
RP	SEQUENCE FROM N.A.				Qy	122 YSQCVVRNLHSQERGMQLQTPOFLCMKALIISIIPVGDKNQKFDELARMYKELDR
RX	MEDLINE=98404133; PubMed=9732460;				Db	746 YSQCVVRNLHSQERGMQLQTPOFLCMKALIISIIPVGDKNQKFDELARMYKELDR
RA	Choong C.S., Kempainen J.A., Wilson E.M.;				Qy	182 IIACKRKNTCSRSRFYVOLTKLDSVOPARELHOFTDLIKSHMVSDFPEMMARIS
RT	"Evolution of the primate androgen receptor: a structural basis for RT disease.";				Db	805 IIACKRKNTCSRSRFYVOLTKLDSVOPARELHOFTDLIKSHMVSDFPEMMARIS
RT	disease.";				Qy	242 VQVKLISKGVKPKIYFHTQ 260
RL	J. Mol. Biol. 27:334-342(1998).				Db	865 VQVKLISKGVKPKIYFHTQ 884
CC	-- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.				Db	866 VQVKLISKGVKPKIYFHTQ 884
CC	-- SUBCELLULAR LOCATION: Nucleus.				RESULT 3	ANDR_MACFA
CC	-- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL STEROID-BINDING DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.				ID	ANDR_MACFA
CC	-- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.				ID	ANDR_MACFA
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between The Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				AC	097952;
CC	EMBL; P06336; IGDC.				DT	30-MAY-2000 (Rel. 39; Created)
CC					DT	30-MAY-2000 (Rel. 39; Last sequence update)
CC					DT	30-MAY-2000 (Rel. 39; Last annotation update)
CC					DB	Androgen receptor (Dihydrotestosterone receptor).
CC					GN	AR OR NR3C4.
CC					OS	Macaca fascicularis (Crab eating macaque) (<i>Cynomolgus monkey</i>).
CC					OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC					OC	Cercopithecidae; Macaca.
CC					OX	NCBI_TaxID=9541;
CC					RN	[1] SEQUENCE FROM N.A.
CC					RP	MEDLINE=98404153; PubMed=9732460;

QY 2 SHMIGEYECOPIFLNLTEIRGVVCAHGHDNNKOPDSFAALISLNGEROLHVRVVKWAK 61
 CC |||||
 Db 638 SH-IEGYECOPIFLNLTEIRGVVCAHGHDNNKOPDSFAALISLNGEROLHVRVVKWAK 696
 CC |||||
 Qy 62 ALPGFERNLHVDDOMAVIQSWMGLNFMAGWRSPTNNSRMLYFAPDLYFNEVRMKRM 121
 CC |||||
 Db 697 ALPGFERNLHVDDOMAVIQSWMGLNFMAGWRSPTNNSRMLYFAPDLYFNEVRMKRM 756
 CC |||||
 Qy 122 YSOCVVRMHLQSBRGMQITPQBLCKMALLSIPPGKLNQKFPEBLRMYIKELDR 181
 CC |||||
 Db 757 YSOCVVRMHLQSBRGMQITPQBLCKMALLSIPPGKLNQKFPEBLRMYIKELDR 816
 CC |||||
 Qy 182 IACKRKNTSCSRPFLKLDSTQPIARLBHQFTFDLKLKSHMSVDPPEMAEIS 241
 CC |||||
 Db 817 IACKRKNTSCSRPFLKLDSTQPIARLBHQFTFDLKLKSHMSVDPPEMAEIS 876
 CC |||||
 Qy 242 VQVKLISGKVKPFIYFQ 260
 CC |||||
 Db 877 VQVKLISGKVKPFIYFQ 895
 CC |||||

RESULT 5
 ANDR MOUSE STANDARD; PRT; 899 AA.
 ID ANDR MOUSE STANDARD; PRT; 899 AA.
 AC F19051;
 DT 01-NOV-1990 (Rel. 16 Created)
 DT 16-OCT-2001 (Rel. 40 Last annotation update)
 DE Androgen receptor (Dihydrotestosterone receptor).
 GN AR OR NR-C4.
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI-TaxID=1090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=90386642; PubMed=2403358;
 RA He W.W., Fischer L.M., Sun S., Bilhartz D.L., Zhu X., Young C.Y.P.,
 RA Kelley D.B., Tindall D.J.;
 RT "Molecular cloning of androgen receptors from divergent species with
 RT a polymerase chain reaction technique: complete cDNA sequence of the
 mouse androgen receptor and isolation of androgen receptor cDNA
 RT probes from dog, guinea pig and clawed frog";
 RL Biochem. Biophys. Res. Commun. 171:697-704(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91133433; PubMed=2178222;
 RA Gaspar M.I., Mao T., Tosi M.;
 RT "Structure and size distribution of the androgen receptor mRNA in
 RT wild-type and Tfm/Y mutant mice";
 RL Mol. Endocrinol. 4:1600-1610(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9135424; PubMed=1883356;
 RA Faber P.W., King A., van Rooij H.C.J., Brinkmann A.O., de Both N.J.,
 RA Trapman J.;
 RT "The mouse androgen receptor. Functional analysis of the protein and
 RT characterization of the gene";
 RL Biochem. J. 278:269-278(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92017874; PubMed=1681426;
 RA Charest N.J., Zhou Z., Lubahn D.B., Olsen K.L., Wilson E.M.,
 RA French F.S.;
 RT "A frameshift mutation destabilizes androgen receptor messenger RNA
 RT in the Tfm mouse";
 RL Mol. Endocrinol. 5:573-581(1991).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC -!- MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
 ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
 HORMONE-BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE
 HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA
 SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 subfamily.

CC ---
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 or send an email to license@isb-sib.ch).

CC ---
 DR EMBL; S65658; AAB9916_1; -;
 DR EMBL; X53779; CA037795_1; -;
 DR EMBL; M17890; AA037234_1; -;
 DR EMBL; X19592; CA042160_1; -;
 DR PIR; A35095; A35835;
 DR HSSP; P06536; 1GDC;
 DR TRANSFAC; T00441; -;
 DR MGB; MGI:88004; AR;
 DR InterPro; IPR001103; Andrgn receptor.
 DR InterPro; IPR000536; Hormone rec lig.
 DR InterPro; IPR001628; Znf_C4teroid.
 DR Pfam; PF02166; Androgen_recep; 1.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STROIDFINGER.
 DR PRODOM; PD000035; Znf_C4teroid; 1.
 DR SMART; SM00430; R011; 1.
 DR SMART; SM0339; ZNF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding; MODULATING (BY SIMILARITY).
 FT DOMAIN 1 537
 FT DNA_BIND 539 604
 FT ZN_FING 539 559
 FT ZN_FING 575 599
 FT C4-TYPE.
 FT DOMAIN 670 899
 FT DOMAIN 63 67
 FT DOMAIN 174 193
 FT DOMAIN 367 373
 FT DOMAIN 391 397
 FT DOMAIN 441 447
 SQ SEQUENCE 899 AA; 98193 MR; FD9EBCT077A568 CRC64;
 Query Match 98.4%; Score 1349.5; DB 1; Length 899;
 Best Local Similarity 99.6%; Pred. No. 3.2e-118;
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 SH-MIGEYECOPIFLNLTEIRGVVCAHGHDNNKOPDSFAALISLNGEROLHVRVVKWAK 61
 CC |||||
 Db 642 SH-IEGYECOPIFLNLTEIRGVVCAHGHDNNKOPDSFAALISLNGEROLHVRVVKWAK 700
 CC |||||
 Qy 62 ALPGFERNLHVDDOMAVIQSWMGLNFMAGWRSPTNNSRMLYFAPDLYFNEVRMKRM 121
 CC |||||
 Db 701 ALPGFERNLHVDDOMAVIQSWMGLNFMAGWRSPTNNSRMLYFAPDLYFNEVRMKRM 760
 CC |||||
 Qy 122 YSOCVVRMHLQSBRGMQITPQBLCKMALLSIPPGKLNQKFPEBLRMYIKELDR 181
 CC |||||
 Db 761 YSOCVVRMHLQSBRGMQITPQBLCKMALLSIPPGKLNQKFPEBLRMYIKELDR 820
 CC |||||
 Qy 182 IACKRKNTSCSRPFLKLDSTQPIARLBHQFTFDLKLKSHMSVDPPEMAEIS 241
 CC |||||
 Db 821 IACKRKNTSCSRPFLKLDSTQPIARLBHQFTFDLKLKSHMSVDPPEMAEIS 880
 CC |||||
 Qy 242 VQVKLISGKVKPFIYFQ 260
 CC |||||
 Db 881 VQVKLISGKVKPFIYFQ 899
 CC |||||

RESULT 6

ID _ANDR RAT	STANDARD;	PRT;	902 AA.
AC P15207; Q63049;	01-APR-1990 (Rel. 14, Last sequence update)		
DT 15-SEP-2003 (Rel. 42, Last annotation update)	DE Androgen receptor (Dihydrotestosterone receptor).		
GN AR OR NR3C4	OS Rattus norvegicus (Rat).		
OC Mammalia; Butheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=10116;	OX [1]		
RP SEQUENCE FROM N.A.	RX MEDLINE=89112209; PubMed=3216867;		
RA Tan J., Joseph D.R., Quarby V.B., Lubahn D.B., Sar M., French F.S., Wilson E.M.;	RT "The rat androgen receptor: primary structure, autoregulation of its messenger ribonucleic acid, and immunocytochemical localization of the receptor protein"; Mol. Endocrinol. 2:1276-1285 (1988).		
RA Wilson E.M.; Chang C., Kokontis J., Liao S.; RT "Structural analysis of complementary DNA and amino acid sequences of human and rat androgen receptors"; Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215 (1988).	RT [13]		
RL Chang C., Kokontis J., Liao S.; RX MEDLINE=90256822; PubMed=2341499;	RN SEQUENCE FROM N.A., AND VARIANT TFM GLN-735.		
RA Yarborough W.G., Quarby V.B., Simental J.A., Joseph D.R., Sar M., Lubahn D.B., Olsen K.L., French F.S., Wilson E.M.; RT "A single base mutation in the androgen receptor gene causes androgen insensitivity in the testicular feminized rat.;" J. Biol. Chem. 265:8903-8900 (1990).	RT		
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.	CC		
CC -!- SUBCELLULAR LOCATION: Nuclear.	CC		
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE SEMINAL VESICLE, VENTRAL PROSTATE AND COAGULATING GLAND WITH LOWER LEVELS IN THE KIDNEY AND LEVATOR ANI MUSCLE.	CC		
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	CC		
CC -!- DISEASE: Defects in AR are a cause of androgen insensitivity. Rates with this syndrome are called testicular feminized (Tfm). CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.	CC		

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RESULT 7

ID _ANDR CANFA	STANDARD;	PRT;	907 AA.
AC Q9T790;	03-MAY-2000 (Rel. 39, Created)		
DT 30-MAY-2000 (Rel. 39, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)		
GN AR OR NR3C4.	DB Androgen receptor (Dihydrotestosterone receptor).		
OS Canis familiaris (Dog).	OC Butheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9615;		
RA Lu B., Smock S.J., Caetleberry T.A., Owen T.A.; RX MEDLINE=21618348; PubMed=11768233;	RT "Molecular cloning and functional characterization of the canine androgen receptor"; Mol. Cell. Biochem. 226:129-140 (2001).		
DR InterPro; IPR00536; Hormone_rec_lig.	CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR		

- Qy 122 YSOCVURMHLSBRPGWLOITPDRFLCKMALLFSIPDGLKQKEFDELMNYKELDR 181
 ID ANDR-HUMAN STANDARD; PRT; 919 AA.
 AC P10275;
 DT 01-MAR-1989 (Rel. 10. Created)
 DT 01-APR-1990 (Rel. 14. Last sequence update)
 DT 15-SEP-2003 (Rel. 42. Last annotation update)
 DE Androgen receptor (Dihydrotestosterone receptor).
 GN AR OR NR3C4 OR DHTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.
 RN [1]—NCBI-TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89112208; PubMed=3216866;
 RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E., French P.S., Wilson E.M., Simental J.A., Higgs H.N., Migeon C.J., RT "Sequence of the intron/exon junctions of the coding region of the human androgen receptor gene and identification of a point mutation in a family with complete androgen insensitivity";
 RL Mol. Endocrinol. 2:1265-1275(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT CA15 MET-866.
 RX MEDLINE=90083302; PubMed=2594783;
 RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J., Wilson E.M., French P.S.; RT "The human androgen receptor: complementary deoxyribonucleic acid cloning, sequence analysis and gene expression in prostate.";
 RL Mol. Endocrinol. 2:1265-1275(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90258935; PubMed=2342476;
 RA Govindan M.V.; RT "Specific region in hormone binding domain is essential for hormone binding and trans-activation by human androgen receptor.";
 RL Mol. Endocrinol. 4:417-427(1990).
 RC TISSUE=prostate;
 RP MEDLINE=8917168; PubMed=3174628;
 RA Chang C., Kokontis J., Liao S.; RT "Structural analysis of complementary DNA and amino acid sequences of human and rat androgen receptors";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8917168; PubMed=3174628;
 RA Giovannucci E., Stampfer M.J., Kriethivas K., Brown M., Dahl D., Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.; RT "The CAG repeat within the androgen receptor gene and its relationship to prostate cancer";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323(1997).
 RN [5]
 RP TISSUE=prostate;
 RX MEDLINE=89098909; PubMed=2911578;
 RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.; RT "Characterization and expression of a cDNA encoding the human androgen receptor";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:3327-3331(1989).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=prostate;
 RA MEDLINE=91115543; PubMed=2293020;
 RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.B., Wilson J.D., McPhaul M.J.;
 RA Sultan C., Lumbroso S., Poujol N., Belon C., Boudon C.,
- RESULT 9
 ANDR-HUMAN STANDARD; PRT; 919 AA.
 AC P10275;
 DT 01-MAR-1989 (Rel. 10. Created)
 DT 01-APR-1990 (Rel. 14. Last sequence update)
 DT 15-SEP-2003 (Rel. 42. Last annotation update)
 DE Androgen receptor (Dihydrotestosterone receptor).
 GN AR OR NR3C4 OR DHTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.
 RN [1]—NCBI-TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89178111; PubMed=3333726;
 RA Chang C., Kokontis J., Liao S.; RT "Molecular cloning of human and rat complementary DNA encoding androgen receptors";
 RL Science 240:324-326(1988).
 RN [8]
 RP SEQUENCE OF 468-919 FROM N.A.
 RX MEDLINE=88240507; PubMed=3377788;
 RA Trapman J., Klaasen P., Kuiper G.G.J.M., van der Korput J.A.G.M., Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voornhorst M.M., Mulder E., Brinkmann A.O.; RT "Cloning, structure and expression of a cDNA encoding the human androgen receptor";
 RL Biochem. Biophys. Res. Commun. 153:241-248(1988).
 RN [9]
 RP INTERACTION WITH RAN.
 RX MEDLINE=99329028; PubMed=10100640;
 RA Heiao P.-W., Lin D.-L., Nakao R., Chang C.; RT "The linkage of Kennedy's neuron disease to AR424, the first identified androgen receptor polyglutamine region-associated coactivator";
 RL J. Biol. Chem. 274:20229-20234(1999).
 RN [10]
 RP POLYMORPHISM OF POLY-GLN REGION.
 RX MEDLINE=92220629; PubMed=1561105;
 RA Sleedens H.F.B.M., Ooster A., Brinkmann A.O., Trapman J.; RT "Trinucleotide repeat polymorphism in the androgen receptor gene (AR).";
 RL Nucleic Acids Res. 20:1427-1427(1992).
 RN [11]
 RP POLYMORPHISM OF POLY-GLN REGION.
 RC TISSUE=Blood;
 RA Lu J., Daniels M.; RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP POLYMORPHISM OF POLY-GLN REGION.
 RX MEDLINE=97250535; PubMed=9096391;
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.; RT "The CAG repeat within the androgen receptor gene and its relationship to prostate cancer";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323(1997).
 RN [13]
 RP ERRATUM.
 RA Giovannucci E., Stampfer M.J., Kriethivas K., Brown M., Dahl D., Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.; RT Proc. Natl. Acad. Sci. U.S.A. 94:8272-8272(1997).
 RN [14]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93093459; PubMed=1458719;
 RA Pisnay L., Trifiro M.A., Kaufman M., Beitel L.K., Mhatre A., Kazemi-Birjani P., Sabbaghian N., Lumbroso R., Alvarado C., Vasiliou M., Gottlieb B.; RT "Androgen resistance due to mutation of the androgen receptor";
 RL Clin. Invest. Med. 15:456-472(1992).
 RN [15]
 RP REVIEW ON VARIANTS ATG.
 RX MEDLINE=93339360; PubMed=8339746;
 RA Brown T.R., Schefer P.A., Chang Y.-T., Migeon C.J., Ghirri P., RA Murono K., Zhou Z.; RT "Molecular genetics of human androgen insensitivity";
 RL Eur. J. Pediatr. 152 Suppl. 2:S62-S69(1993).
 RN [16]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=9405970; PubMed=8240973;
 RA Sultan C., Lumbroso S., Poujol N., Belon C., Boudon C.,

MACIES	
RT	"Mutations of androgen receptor gene in androgen insensitivity syndromes";
RT	J. Steroid Biochem. Mol. Biol. 46:519-530(1993).
[17]	
RR	REVIEW ON VARIANTS
RX	MEDLINE=95033089; PubMed=7337057;
RA	Patterson M.N., Hughes I.A., Gottlieb B., Pinsky L.;
RT	"The androgen receptor gene mutations database.";
RL	Nucleic Acids Res. 22:3560-3562(1994).
RN	[18]
RP	REVIEW ON VARIANTS
RX	MEDLINE=95532489; PubMed=7636493;
RA	Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korput J.A.G.M., Bruggenwirth H.T., Boehmer A.L.M., Trapman J.;
RT	"Androgen receptor mutations.";
RL	J. Steroid Biochem. Mol. Biol. 53:443-448(1995).
RN	[19]
RP	REVIEW ON VARIANTS
RX	MEDLINE=97169385; PubMed=9016528;
RA	Gottlieb B., Triifiro M.A., Lumbrico R., Vasiliou D.M., Pinsky L.;
RT	"The androgen receptor gene mutations database.";
RL	Nucleic Acids Res. 25:158-162(1997).
RN	[20]
RP	VARIANT LNCAP ALA-877.
RX	MEDLINE=91083633; PubMed=2260966;
RA	Veldscholte J., Ris-Stalpers C., Kuiper G.G.J.M., Jenster G., Berrevoets C.A., Claassen E., van Rooij H.C.J., Trapman J., Brinkmann A.O., Mulder E.;
RT	"A mutation in the ligand binding domain of the androgen receptor of human LNCAP cells affects steroid binding characteristics and response to anti-androgens.";
RT	Biochem. Biophys. Res. Commun. 173:534-540(1990).
RN	[21]
RP	VARIANT CATS CYS-774; GLN-831 AND MET-866.
RX	MEDLINE=91186983; PubMed=2082179;
RA	Brown T.R., Lubahn D.B., Wilson B.M., French P.S., Migeon C.J., Corfen J.L.;
RT	"Functional characterization of naturally occurring mutant androgen receptors from subjects with complete androgen insensitivity.";
RL	Mol. Endocrinol. 4:1759-1772(1990).
RN	[22]
RP	VARIANT CYS-774.
RX	MEDLINE=91310758; PubMed=1856263;
RA	Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D., McPhaul M.J.;
RA	"Androgen resistance associated with a mutation of the androgen receptor at amino acid 772 (Arg-->Cys) results from a combination of decreased messenger ribonucleic acid levels and impairment of receptor function.";
RT	J. Clin. Endocrinol. Metab. 73:318-325(1991).
RN	[23]
RP	VARIANT CAIS PRO-617.
RX	MEDLINE=91154385; PubMed=1999491;
RA	McPhaul M.J., Zoppi S., Grino P., Griffin J.E., Wilson J.D., Marcelli M., Zoppi S., Grino P., Griffin J.E., Wilson J.D.;
RA	"A mutation in the DNA-binding domain of the androgen receptor gene causes complete testicular feminization in a patient with receptor-positive androgen resistance.";
RT	J. Clin. Invest. 87:1123-1126(1991).
RN	[24]
RP	VARIANT PAYS CYS-763.
RX	MEDLINE=91185626; PubMed=2010552;
RA	McPhaul M.J., Marcelli M., Tilley W.D., Griffin J.E., Isidro-Gutierrez R.P., Wilson J.D.;
RT	"Molecular basis of androgen resistance in a family with a qualitative abnormality of the androgen receptor and responsive to high-dose androgen therapy.";
RT	J. Clin. Invest. 87:1413-1421(1991).
RN	[25]
RR	RESULT 10
ID	PRGR_RABIT
PRGR_RABBIT	STANDARD:
PRT	930 AA.
AC	P06186;
DT	01-JAN-1988 (Rel. 06, Created)
DT	01-JAN-1988 (Rel. 06, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DR	Progesterone receptor (PR).
GN	PGK OR NR3C3.
OS	Oryctolagus cuniculus (Rabbit)
OC	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=87067449; PubMed=3538016;
RA	Löösfelt H., Atger M., Misrahi M., Guiochon-Mantel A., Meriel C., Losset F., Benarous R., Milgrom E.;
RT	"Cloning and sequence analysis of rabbit progesterone-receptor complementary DNA.";
RL	Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
CC	-1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC	--1- SUBCELLULAR LOCATION: nuclear.
CC	--1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN
CC	--1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
CC	[26]
DR	EMBL; M14547; A831443.1; -.
DR	PIR; A25923; A25923.
DR	HSSP; P06401; 1A2B
DR	TRANSFAC; T00697; -.
DR	InterPro; IPR00516; Hormone_rec_lig.
DR	InterPro; IPR00128; Progest_receptor.
DR	InterPro; IPR00128; Znf_Cxteroid.
DR	InterPro; IPR001628; Znf_Cxteroid.
DR	Pfam; PF00104; hormone_rec; 1.
DR	PFAM; PF002161; Prog_receptor; 1.
DR	PRINTS; PF00598; STARDHORMONER.

DR PRINTS: PR00047; STROIDFINGER.
 DR Prodrom, PD00035, Znf_C4steroid, 1.
 DR SMART; SM00330; Holi; 1.
 DR PROSITE; PS00031; NUCLEAR_PCEPTOR; 1;
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW C4-finger; Steroid-binding.
 FT DOMAIN 1 565 MODULATING, PRO-RICH.
 FT DNA_BIND 568 633 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 568 588 C4-TYPE.
 FT ZN_FING 604 628 C4-TYPE.
 FT DOMAIN 678 930 STEROID-BINDING.
 FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 930 AA: 98666 MW; 644FFAC13BF2F883 CRC64;

Query Match 55.9%; Score 766; DB 1; Length 930;
 Best Local Similarity 55.5%; Pred. No. 1.2e-63; Mismatches 53; Indels 0; Gaps 0;
 Matches 137; Conservative 57; MisMatches 53; Insert 0; Gap 0;

Ov 12 PIFLNLVIAEPEPGVAGHNNQDPSPAUSSLNELGRQEVHVVKAALPGFRHLHV 71
 Db 682 PPLNLNSIBPPVDTSSLLSINQGRQLSVWMSKPGFRHLH 741

Ov 72 DDOAVQYQSMWGLMVANGWTSFTNVNSRMLYFAPDILVFNTRMHSRMYQCVRMHHL 131
 Db 742 DQITLIQYQSWMSLMLVFGIIGWASQKHSQGQMLIFAPPDLINFORMKESSTFSICLWQI 801

Ov 132 SRRPGWQITPREFLCAALUFLSIIPVGDKNKFDELRLANVYKEDRIRACKKNT 191
 Db 802 PDBFKLQLQSREBLCKWVLLIANTIPLEGLUSOSOFBEMRSVYIRELIKAGLROKGV 861

Ov 192 SSRRYQLTQKLDSDVQPIARELHQFTDILKSHMWSVDPEMMARISVQPKLISGK 251
 Db 862 SSSRQYQLTQKLDSDVQPIARELHQFTDILKSHMWSVDPEMMARISVQPKLISGK 921

Ov 252 VPKYFH 258

Ds 922 VPKYFH 928

RESULT 11

PRGR_HUMAN ID _BGR_HUMAN STANDARD; PRT: 933 AA.

AC P06401; Q8IPF7;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 16-SEP-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DB Progesterone receptor (PR).
 GN PRGR OR NR3C3.
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RX MEDLINE=9228361; PubMed=2328727;
 RA Kastner P.; Krust A.; Turcotte B.; Stroop U.; Tora L.; Gronemeyer H.;
 RA Champom P.;
 RT "Two distinct estrogen-regulated promoters generate transcripts
 encoding the two functionally different human progesterone receptor
 genes A and B";
 RL EMBO J. 9:1603-1614(1990).

RN [2] SEQUENCE FROM N.A.

RX MEDLINE=8718455; PubMed=3551956;
 RA Misrahi M.; Auger M.; D'Auriol L.; Loosfelt H.; Meriel C.';
 RA Fridlansky P.; Guiolard-Mantel A.; Galibert F.; Milgrom E.';
 RT "Complete amino acid sequence of the human progesterone receptor
 deduced from cloned cDNA";
 RL Biochem. Biophys. Res. Commun. 143:740-748(1987).
 RN [3] SEQUENCE FROM N.A.
 RA Kleback D.G.; Agoulnik I.U.; Tong X.-W.;

RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933.
 RX MEDLINE=9828128; PubMed=9620806;
 RA Williams S.P.; Sigler P.B.;"Atomic structure of progesterone complexed with its receptor.";
 RT Nature 393:392-396(1998).
 RL -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -1- SUBCELLULAR LOCATION: nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoform=2;
 CC Name_A; IsoID=P06401-1; Sequence=Displayed;
 CC IsoID=P06401-2; Sequence=VSP_003706;
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to licensee@isb-sib.ch).

DR EMBL; X51730; CRA36018.1; -;
 DR EMBL; M15716; AAA60081.1; -;
 DR EMBL; AF016381; AA001587.1; -;
 DR PIR; S09971; QRHUP;
 DR PDB; 1A28; 15-JUL-98.
 DR PDB; 1E3K; 14-JUN-01.
 DR TRANSFAC; T00596; -;
 DR Genew; HGNC:8910; PGR.
 DR MIM; 607311; -;
 DR MIM; 264080; -;
 DR GO; GO:0003707; P:steroid hormone receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR00536; Hormone rec_lig.
 DR InterPro; IPR00128; Progest receptor.
 DR InterPro; IPR001723; Sidham_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF02161; Prog_rec; 1.
 DR Pfam; PF00105; zf_C4; 1.
 DR PRINTS; PR00038; STROIDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR Prodrom; PD00035; Znf_C4steroid; 1.
 DR SMART; SM00430; Holi; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding; Phosphorylation; Alternative splicing;
 KW 3D-structure; Polymorphism.
 FT DOMAIN 1 566 MODULATING, PRO-RICH.
 FT DNA_BIND 567 632 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 567 587 C4-TYPE.
 FT ZN_FING 603 627 C4-TYPE.
 FT DOMAIN 681 933 STEROID-BINDING.
 FT DOMAIN 183 187 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 41 41 PHOSPHORYLATION (BY CK).
 FT MOD_RES 227 227 PHOSPHORYLATION (BY CK).
 FT MOD_RES 232 232 PHOSPHORYLATION (BY CK).
 FT MOD_RES 552 552 PHOSPHORYLATION (BY CK).
 FT MOD_RES 793 793 PHOSPHORYLATION (BY CK).
 FT VARSPlic 1 164 Missing (in Isoform A).
 FT /PRD=var 003706.
 FT VARIANT 625 625 R -> I (IN dbSNP:2020874).

PT	VARIANT	865	865	/PfamId=PAR 014627; S -> L (IN dbSNP-2020880). OX	OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_Taxid=10116;
PT	CONFFLICT	226	226	G -> S (IN REF. 1).	RN [1]
PT	CONFFLICT	256	256	V -> S (IN REF. 1).	RP SEQUENCE FROM N.A.
PT	CONFFLICT	344	344	S -> T (IN REF. 1).	RC STRAIN=Sprague-Dawley; TISSUE=Placenta;
PT	CONFFLICT	660	660	L -> V (IN REF. 2).	RX MEDLINE=94130817; PubMed=8229566;
PT	HELIX	686	693	RT Park-Sarge O.K.; Mayo K.B.;	RA
PT	TURN	694	694	RT "Regulation of the progestosterone receptor gene by gonadotropins and cyclic adenosine 3',5'-monophosphate in rat granulosa cells.";	RT
PT	HELIX	711	735	RT Endocrinology 134:709-718 (1994).	RL
PT	TURN	737	738	CC -I- FUNCTION: THB STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.	CC
PT	HELIX	739	741	CC -I- SUBCELLULAR LOCATION: Nuclear.	CC
PT	TURN	744	770	CC -I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	CC
PT	STRAND	772	773	CC -I- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.	CC
PT	TURN	775	779	CC -----	CC
PT	TURN	780	781	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.sib.ch/announce/ or send an email to license@ebi.sib.ch).	CC
PT	STRAND	782	785	CC -----	CC
PT	HELIX	786	790	CC -----	CC
PT	TURN	791	791	CC -----	CC
PT	HELIX	795	811	CC -----	CC
PT	TURN	812	812	CC -----	CC
PT	HELIX	815	826	CC -----	CC
PT	TURN	827	827	CC -----	CC
PT	STRAND	829	830	CC -----	CC
PT	TURN	832	833	CC -----	CC
PT	TURN	836	837	CC -----	CC
PT	HELIX	838	857	CC -----	CC
PT	TURN	858	859	CC -----	CC
PT	HELIX	863	896	CC -----	CC
PT	TURN	897	897	CC -----	CC
PT	HELIX	902	901	CC -----	CC
PT	TURN	907	921	CC -----	CC
PT	TURN	922	923	CC -----	CC
PT	STRAND	926	927	CC -----	CC
SQ	SEQUENCE	933	AA:	98994 MW: 80414B7P1F317P93 CRC64:	DR
Query Match 55.8%; Score 765; DB 1; Length 933;					
Best Local Similarity 55.5%; Pred. No. 1 5e-63; Mismatches 53; Indels 0; Gaps 0;					
Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;					
Qy	12 PFLANVLRAIRPEGVWCAHGDDNNQPSFAALLSFVNSRMLYFAPDLVNEYRMHKSRSMSQCVRMHLV 71	685	PPLINLMSIPLDPVIVACHDNTKPDTSLLTSNLQGEROLISUVKWSKSPGFRNLHI 744	PRINTER; PR000536; Hormone rec lig.	DR
Db	72 DDMAVIQYSWGMGLMVRAMGMSFTNNSRMLYFAPDLVNEYRMHKSRSMSQCVRMHLV 131	745	DQDTLQYSWMSLMVFGLGWSYKHSQMYFAPDLVNEYRMHKSRSMSQCVRMHLI 804	INTERPRO; IPRO00128; Progesterone receptor.	DR
Qy	132 SOBFGWQTIPQPFCLMKALLSFITPVGLKNQFKEDLRNMYKLDRITACKRNPT 191	805	PRBFVKLQVSOPBFCLMKVLLNLTIPLEGLSQTOFEEMRSYIRELIKAGLQRKGVV 864	INTERPRO; IPRO00123; Steroid receptor.	DR
Db	192 SCSRRYVQLTKLSDVQPIARSHKQHTFDLKLKSHMSVDPREMMARISVQVKPLSGK 251	865	SBSQRFYQVTKLQDNLHDVQLQHLYCLNTPFIOSRALSVEPFMMSEVIAQOLPKILGM 924	SMART; SM00430; HOXI-1; SMART; SM00393; ABP_C4_1.	DR
Qy	252 VPKIYH 258	925	VPKIYH 931	DR PROSTE; PS00031; NUCLEAR RECEPTOR; 1.	DR
Db	RESULT 12	925	VPKIYH 931	KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; ZINC-finger; Steroid-binding DOMAIN 1 556	DR
PRGR_RAT	STANDARD	923	FT ZN_FING 557 622 NUCLEAR RECEPTOR-TYPE.	ZINC-finger; Steroid-binding DOMAIN 1 556	DR
ID_PRGR_RAT		923	FT ZN_FING 557 622 NUCLEAR RECEPTOR-TYPE.	DNA BIND	DR
AC_063449;		923	FT DOMAIN 671 923 STEROID-BINDING.	FT DOMAIN 671 923 STEROID-BINDING.	DR
DT 20-MAY-2000 (Rel. 39, Created)		923	FT DOMAIN 104 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).	FT DOMAIN 104 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).	DR
DT 30-MAY-2000 (Rel. 39, Last Sequence update)		923	SQ SEQUENCE	SEQUENCE	DR
DT 20-MAY-2000 (Rel. 39, Last annotation update)		923	Query Match 55.4%; Score 755; DB 1; Length 923;	923 AA: 99407 MW: 05384B9656BF22DC CRC64;	DR
PRGesterone receptor (PR)		923	Best Local Similarity 55.5%; Pred. No. 5.5e-63; Mismatches 55; Indels 0; Gaps 0;	923 AA: 99407 MW: 05384B9656BF22DC CRC64;	DR
GN PRG OR NR3C3		923	Qy 12 PFLANVLRAIRPEGVWCAHGDDNNQPSFAALLSFVNSRMLYFAPDLVNEYRMHKSRSMSQCVRMHLV 71	675 PPLINLMSIPLDPVIVACHDNTKPDTSLLTSNLQGEROLISUVKWSKSPGFRNLHI 734	DR
OS Rattus norvegicus (Rat)		923	Db 735 DQDTLQYSWMSLMVFGLGWSYKHSQMYFAPDLVNEYRMHKSRSMSQCVRMHLI 794	132 SOBFGWQTIPQPFCLMKALLSFITPVGLKNQFKEDLRNMYKLDRITACKRNPT 191	DR
Batrachota; Craniata; Vertebrata; Euteleostomi;		923	795 PRBFVKLQVSOPBFCLMKVLLNLTIPLEGLSQTOFEEMRSYIRELIKAGLQRKGVV 854	192 SCSRRYVQLTKLSDVQPIARSHKQHTFDLKLKSHMSVDPREMMARISVQVKPLSGK 251	DR
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		923	855 PSSQRFYQVTKLQDNLHDVQLQHLYCLNTPFIOSRALSVEPFMMSEVIAQOLPKILGM 914		DR

RESULT 13

PRGR_MOUSE . STANDARD; PRT; 923 AA.

ID PRGR_MOUSE . STANDARD; PRT; 923 AA.

AC 000175;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DR progestrone receptor (PR).

GN PRGR OR NRJ3 OR PR.

OS Mus musculus. (Mouse).

OC Mammalia; Batheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91289759; PubMed=2069958;

RA Schott D.R., Shyamala G., Schneider W., Parry G.;

RT "Molecular cloning, sequence analyses, and expression of complementary DNA encoding murine progestrone receptor.", Biochemistry 30:7014-7020(1991).

RN [2]

RP SEQUENCE OF 1-9 FROM N.A.

RX STRAIN=129/Sv;

RX MEDLINE=95100931; PubMed=7802637;

RA Hagiwara K., Wu-Peng X.S., Funabashi T., Kato J., Pfaff D.W.;

RT "Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the mouse progestrone receptor gene.", Biochem. Biophys. Res. Commun. 205:1093-1101(1994);

CC -- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -- SUBCELLULAR LOCATION: Nuclear.

-- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

-- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.

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CC

RESULT 14

PRGR_CHICK . STANDARD; PRT; 786 AA.

ID PRGR_CHICK . STANDARD; PRT; 786 AA.

AC P07812; Q90946;

DT 01-AUG-1988 (Rel. 08, Created)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DR Progestrone receptor (PR).

GN PRGR OR NRJ3C.

OS Gallus gallus (Chicken).

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TAXID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8116640; PubMed=3441098;

RA Gronemeyer H., Tuccotte B., Quirin-Stricker C., Bocquel M.T., Meyer M.B., Krozowski Z., Jeitsch J.M., Lerouge T., Garnier J.M., Chamont P.,

RT "The chicken progestrone receptor: sequence, expression and functional analysis.", EMBO J. 6:3985-3994(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91042592; PubMed=3153474;

RA Connelly O.M., Dobson A.D.W., Tsai M.-J., Beattie W.G., Toft D.O., Huckabay C.S., Zarecki T., Schrader W.T., O'Malley B.W.;

RT "Sequence and expression of a functional chicken progestrone receptor.", Mol. Endocrinol. 1:517-525(1987).

RN [3]

RP SEQUENCE OF 128-164 FROM N.A.

RX MEDLINE=86288413; PubMed=2226779;

RA Connelly O.M., Sullivan W.P., Sillitoe D.O., Birnbaumer M., Cook R.G., Maxwell B.L., Zarucki-Schulz T., Greene G.I., Schrader W.T., O'Malley B.W.;

RT "Molecular cloning of the chicken progestone receptor.", Science 233:767-770(1986).

RN [4]

RP SEQUENCE OF 417-499 FROM N.A.

RN [1]

RP 556 MODULATING, PRO-RICH.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Ruthereria; Getaridoactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN NCBI-TAXID:9940;
 [1] -
 RP SEQUENCE FROM N.A.

RC STRAIN=Romanov; TISSUE=Uterus;
 RA Madigou T., Tiffache C., Le Gall F., Pelletier J., Thieulant M.;
 RL Submitted '(SBP-1997)' to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC

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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC

CC BMLB; Z65555; CAA91447.1; -.

DR HSSP; P0401; I428.

DR InterPro; IPR000536; Hormone_rec_lig.

DR InterPro; IPR00128; Progest_Receptor.

DR InterPro; IPR001723; Steroid_Receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR PFAM; PF00104; hormone_rec; 1.

DR PFAM; PF02161; Prog_receptor; 1.

DR PFAM; PF00105; zf-C4; 1.

DR PRINTS; PRO0398; STRODHORMONER.

DR PRINTS; PRO0047; STEROIDFINGER.

DR SMART; SM00430; HOLT; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.

DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.

DR ZINC; ZINCPING; Zinc_Finger; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;

KW Zinc-Finger; Steroid-binding.

FT NON_TER 1 1 MODULATING, PRO-RICH.

FT DOMAIN <1 15 NUCLEAR RECEPTOR-TYPE.

FT DNA_BIND 18 83 C4-TYPE.

FT ZN_PING 18 38 C4-TYPE.

FT ZN_PING 54 78 C4-TYPE.

FT DOMAIN 128 >377 STEROID-BINDING.

FT NON_TER 377 377

SQ SEQUENCE 377 AA; 42904 MW; 3141B65587P7493C CRC64;

Query Match 53.8%; Score 739; DB 1; Length 377;
 Best local Similarity 55.0%; Pred. No. 1.6e-61; Mismatches 52; Indels 0; Gaps 0;
 Matches 133; Conservative 57;

Qy 12 PFLAVNLAEIPGVCAHGDNQDSFAALLSLNBLGERQLIVVVKWAKALGFRNLAV 71
 136 PPLINTLMSIEPDVMYAGHDNSKDTSLLTSINOLGERQLSVKNSKFGRNLAVI 195
 Qy 72 DDDQMAVIQSWMMGLMVFANGWRSPTVNNSRMLVAPDLYFNEYTKHKNRYSQCVRMHHL 131
 196 DDDQTLIQSWMMGLMVFANGWRSPTVNNSRMLVAPDLYFNEYTKHKNRYSQCVRMHHL 255
 Db 132 S0ERGWLOITPQBTLCMRKALLSIIIPVGKQKPFDPDLMYTKEDRICKRKP 191
 256 PQSERVKLQLSQBERLICMKYLLLNTIPGLRSRNQFERMSVIREKAIKQURQKV 315
 192 SCRRPYQLTKLIDSVPARELHQFTPDLLIKSHMVSDPPEMAETISVQPKLUSKG 251
 316 PSSORFYQLTKLUDLNDLVLQKQHLYCLNTPIQSRLSVEPPMSVIAQPKLILGM 375
 Qy 252 VK 253

Db 376 VR 377
 |||
 Search completed: October 9, 2003, 11:41:31
 Job time : 12 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 9, 2003, 11:40:28 ; Search time 19 Seconds
(without alignments)

Perfect score: US-09-687-609a-1

Sequence: I GSHMTB3YBCQPIFLNLEA..... SVQVPLKLSGVKPVYFHTQ 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283308 seqs, 96188682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 7.6.*

1: pix1:*

2: pix2:*

3: pix3:*

4: pix4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1349.5	98.4	899 2	A35895 androgen receptor - mouse
2	1349.5	98.4	902 2	B40494 androgen receptor
3	1349.5	98.4	919 2	A39248 androgen receptor
4	1341.5	97.8	910 2	A34721 androgen receptor
5	1305	95.3	911 2	B34721 androgen receptor
6	1217	88.8	344 2	151330 androgen receptor
7	900	65.6	848 2	JG0194 androgen receptor
8	766	55.9	930 2	A25923 androgen receptor
9	765	55.8	933 1	ORHUP androgen receptor
10	759	55.4	923 2	I532B0 androgen receptor
11	758	55.3	923 2	A39596 androgen receptor
12	752	54.9	786 2	A35466 androgen receptor
13	665	48.5	984 2	A25913 androgen receptor
14	662.5	48.3	777 1	ORHUGA androgen receptor
15	662	48.3	981 1	A41401 androgen receptor
16	657.5	48.0	783 1	A25691 androgen receptor
17	650.5	47.4	776 1	S44047 androgen receptor
18	648.8	47.3	758 2	S60586 androgen receptor
19	644.5	47.0	771 2	A54273 androgen receptor
20	638.5	46.6	795 1	ORRTG androgen receptor
21	564	41.1	742 1	QRHUGB androgen receptor
22	387	28.2	166 2	S35795 androgen receptor
23	285	20.9	110 2	I532B7 androgen receptor
24	222	16.2	535 2	S58224 androgen receptor
25	218.5	15.9	589 1	ORCHE androgen receptor
26	218	15.9	1 ORXLE androgen receptor	
27	216.5	15.8	595 2	I47140 androgen receptor
28	214.5	15.7	620 2	T10423 androgen receptor
29	214.5	15.6	574 2	A37197 androgen receptor

ALIGNMENTS

	30	213.5	15.6	599 1	ORMSE estrogen receptor
31	211.5	15.4	600 1	ORRTE estrogen receptor	
32	207.5	15.1	503 2	JW0046 estrogen receptor	
33	204.5	14.9	595 1	ORHRE estrogen receptor	
34	204.5	14.9	701 2	S64737 estrogen receptor	
35	203.5	14.8	477 2	S71400 estrogen receptor	
36	203.5	14.8	530 2	J05939 RXR type hormone receptor	
37	197	14.4	462 2	S44490 steroid hormone receptor	
38	171	12.5	521 2	A22345 steroid hormone receptor	
39	170	12.4	433 2	B2345 estrogen receptor	
40	168	12.3	433 2	S58087 steroid hormone receptor	
41	148.5	10.8	461 1	A44077 nuclear steroid/throid hormone receptor	
42	148.5	10.8	808 1	S31708 steroid hormone receptor	
43	145.5	10.6	462 2	A40716 steroid hormone receptor	
44	145	10.6	462 1	A56120 steroid hormone receptor	
45	10.4		463 2	S26670 retinoic acid receptor	

A; Residues: 366-413 <HEW>; EMBL:X53779
 A; Cross-references: GB:M20133; NID:202895; PTID:AAA40733_1; PID:920296
 R; Gaspar, M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991
 A; Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived
 A; Reference number: 149501; MUID:92220902; PMID:1924321
 A; Accession: 149501
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 R; Molcule type: mRNA
 A; Residues: 1-899 <RES>
 A; Cross-references: GB:M37890; NID:9191935; PTID:AAA37234_1; PID:9191936
 C; Genetics:
 A; Introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 849/3
 C; Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C; Keywords: DNA binding; transcription regulation; zinc finger
 F; 1-565/Domain: regulatory #status predicted <REG>
 F; 537-795/Domain: erba transforming protein homology <ERBA>
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 F; 575-899/Domain: hormone binder #status predicted <LIG>
 Query Match 98.4%; Score 1349.5; DB 2; Length 899;
 Best Local Similarity 99.6%; Pred. No. 2.5e-118; Mismatches 0; Indels 1; Gaps 1;
 Matches 258; Conservative 0;
 Qy 2 SHMIEGKSYCOPITFLNVLAEISPGVCAHGHDNNQDPSFAALASLNLGEROLVHVTWAK 61
 Db 642 SH-IEGTECQPFIFLNVLAEISPGVCAHGHDNNQDPSFAALASLNLGEROLVHVTWAK 700
 Qy 62 ALPGFERMLHVDDOMAVIQYSWGMILVAMGWRSPTNNSRMYFADPLVYEVYMEKSRM 121
 Db 701 ALPGFERMLHVDDOMAVIQYSWGMILVAMGWRSPTNNSRMYFADPLVYEVYMEKSRM 760
 Qy 122 YSQCVRMHLHSQRFGLQITPQBLCKMALLFSIPDGLKNGQKFEDLRANYIKELDR 181
 Db 761 YSQCVRMHLHSQRFGLQITPQBLCKMALLFSIPDGLKNGQKFEDLRANYIKELDR 820
 Qy 182 IACKRKNPSCSRRFYQQLKLSVQPTARELMOPTFDLLIKSHMSVDPEMMARITS 241
 Db 821 IACKRKNPSCSRRFYQQLKLSVQPTARELMOPTFDLLIKSHMSVDPEMMARITS 880
 Qy 242 VQVPKILSGKVPKIYFHTQ 260
 Db 881 VQVPKILSGKVPKIYFHTQ 260
 Qy 881 VQVPKILSGKVPKIYFHTQ 899

RESULT 2

B40494 androgen receptor - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text_change 20-Sep-1999
 C; Accession: B40494; A34933; A66283; B40108
 R; Chang, C.; Koliakis, J.; Liao, S.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
 A; Title: Structural analysis of complementary DNA and amino acid sequences of human and
 A; Reference number: A40494; MUID:89017168; PMID:3174628
 A; Accession: B40494
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-902 <CH>
 A; Cross-references: GB:M2324; NID:9202957; PTID:AAA40759_1; PID:9202958
 R; Tan, J.; Joseph, D.R.; Quaraby, V.E.; Lubahn, D.B.; Sar, M.; French, P.S.; Wilson, B.M.
 Mol. Endocrinol. 2, 1276-1285, 1988
 A; Title: The rat androgen receptor: primary structure, autoregulation of its messenger
 A; Reference number: A34943; MUID:89112209; PMID:3216867
 A; Accession: A34943
 A; Molecule type: mRNA
 A; Residues: 1-388, 'S', 390-902 <TAN>
 A; Cross-references: GB:M20133; NID:202895; PTID:AAA40733_1; PID:920296
 R; Yarbrough, W.G.; Quaraby, V.E.; Simental, J.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; C
 J. Biol. Chem. 265, 8893-8900, 1990
 A; Title: A single base mutation in the androgen receptor gene causes androgen insensitiv
 A; Reference number: A36283; MUID:90256822; PMID:2241409

RESULT 3

A39248 androgen receptor - human
 C; Species: Homo sapiens (man)
 C; Date: 04-Oct-1991 #sequence revision 04-Oct-1991 #text_change 24-Nov-1999
 C; Accession: A39248; A35328; A4009; A60945; A3942; A27653; A0108; A4094; A32224; A40
 R; Lubahn, D.B.; Brown, T.R.; Simmental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, B.M.; Fr
 Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
 A; Title: Sequence of the intron/exon junctions of the coding region of the human androge
 A; Reference number: A39248; MUID:90083302; PMID:2594783
 A; Accession: A39248
 A; Molecule type: DNA
 A; Residue: 1-919 <LUB>
 A; Cross-references: GB:M27423; GB:M27430; NID:9178904; PTID:AAA51886_1; PID:9178905
 R; Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkmann,
 Mol. Cell. Endocrinol. 61, 257-262, 1989
 A; Title: The N-terminal domain of the human androgen receptor is encoded by one, large e
 A; Reference number: A30328; MUID:89137730; PMID:2917688
 A; Accession: A30328
 A; Molecule type: DNA
 A; Residue: 1-77, 79-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>
 A; Cross-references: GB:M20260
 R; Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, P.S.; Wilson, B.M.
 Science 240, 327-330, 1988
 A; Title: Cloning of human androgen receptor complementary DNA and localization to the X
 A; Reference number: A40109; MUID:88178112; PMID:3353727
 A; Accession: A40109
 A; Molecule type: DNA
 A; Residue: 559-624 <LJZ>
 A; Cross-references: GB:M20132

R; Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Rib-Stalpe, J.; Mol. Endocrinol. 2, R1-R4, 1989
A; Title: Structural organization of the human androgen receptor gene.
A; Reference number: A60946; MUID:89322749; PMID:2546571
A; Accession: A60946
A; Molecule type: DNA
A; Residues: 536-540,587-591,626-631,723-726,770-774,814-818,867-970 <XMT>
R; Lubahn, D.B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, P.S.; Mol. Endocrinol. 2, 1265-1275, 1988
A; Title: The human androgen receptor: complementary deoxyribonucleic acid cloning, sequence and expression of a cDNA encoding the human androgen receptor
A; Accession: A34942
A; Molecule type: mRNA
A; Residues: 1-919 <LU3>
A; Cross-references: GB:M20132; NID:9178627; PMID:AAA51729.1; PID:9178628; GB:J03180
R; Trampont, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.; van Bichem, Biophys. Rev. Commun. 153, 241-248, 1988
A; Title: Cloning, structure and expression of a cDNA encoding the human androgen receptor
A; Accession: A27653; MUID:89340407; PMID:3377788
A; Molecule type: mRNA
A; Residues: 468-564, 'K', 566-919 <TRA>
A; Cross-references: GB:M20260; NID:9178891; PMID:AAA51774.1; PID:9178892
A; Note: the authors translated the codon AAG for residue 565 as Glu
R; Chang, C.; Kokontis, J.; Liao, S.
A; Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor
A; Reference number: A40108; MUID:89178111; PMID:3353726
A; Accession: A40108
A; Molecule type: mRNA
A; Residues: 557-628 <CHA>
A; Cross-references: GB:M8624
R; Chang, C.; Kokontis, J.; Liao, S.
Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
A; Title: Structural analysis of complementary DNA and amino acid sequences of human and A; Reference number: A40494; MUID:89017168; PMID:3174628
A; Accession: A40494
A; Molecule type: mRNA
A; Residues: 1-74, 79-89, 'H', 90-472, 'GGG', 473-474, 'E', 476-644, 'N', 646-919 <CH2>
R; Tilley, W.D.; Marcelli, M.; Wilson, J.D.; McPhaul, M.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 327-331, 1989
A; Title: Characterization and expression of a cDNA encoding the human androgen receptor.
A; Reference number: A32224; MUID:89098909; PMID:2911578
A; Accession: A32224
A; Molecule type: mRNA
A; Residues: 1-77, 79-211, 'R', 213-471, 473-919 <TIL>
A; Cross-references: GB:M01748; GB:J04150; NID:9178871; PMID:AAA51771.1; PID:9178872
R; Mowczowicz, I.; Lee, H.T.; Mestayer, C.; Portois, M.C.; Cabrol, S.; Mauvaz, Mol. Endocrinol. 7, 861-869, 1993
A; Title: A point mutation in the second zinc finger of the DNA-binding domain of the androgen receptor
A; Reference number: A40715; MUID:94019395; PMID:8413310
A; Accession: A40715
A; Species: Homo sapiens (man)
A; Residues: 557-614, 'H', 616-624 <MOW>
A; Cross-references: PIDN:AB28340.1; PID:9425580
C; GeneID: 1190
A; Gene: GDB:AR
A; Cross-references: GDB:120556; OMIM:313700
A; MDP position: Xq11-Xq12
A; Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3
C; Superfamily: unassigned erba-related proteins; erba transforming protein homology
C; Keywords: DNA binding; steroid binding; transcription regulation; zinc finger
F; 557-815; Domain: erba transforming protein homology <ERBA>
F; 559-579; Region: zinc finger
F; 595-619; Region: zinc finger

RESULT 4
A34721
androgen receptor A - human
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C; Accession: A34721
R; Govindan, M.V.
Mol. Endocrinol. 4, 417-427, 1990
A; Title: Specific region in hormone binding domain is essential for hormone binding and A; Reference number: A34721; MUID:90258935; PMID:2342476
A; Molecule type: mRNA
A; Residues: 1-910 <GOV>
C; Superfamily: unassigned erba-related proteins; erba transforming protein homology F; 598-806; Domain: erba transforming protein homology <ERBA>
F; 559-570; Region: zinc finger
F; 586-610; Region: zinc finger

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Matches 256; Conservative 98.8%; Pred. No. 1.4e-117; Indels 1; Gaps 1;
Mismatches 1; Similarity 98.8%;
Query 2 SHMTTEGYEGQPIFNLAEIEPGWCAQDNNQPSFALLSSNLGERQHVKMK 61
Db 653 SH-TEGYEGQPIFLNLAEIEPGWCAQDNNQPSFALLSSNLGERQHVKMK 711
Db 712 ALPGRMLNDQDMAVIQGIGWGMNPAANGWRSPINVSRLMFAPDLYFNETRMKSM 121
Db 712 YSQCVMRHLISQEGWLOITPOBFLCMKMLLSSIIIPVQGLKNQKFPRDELMYTKELR 181
Db 772 YSQCVMRHLISQEGWLOITPOBFLCMKMLLSSIIIPVQGLKNQKFPRDELMYTKELR 831
Db 182 IIACKRKNTSCSRFYQPTKLNSVQPARLHQFTDPLTLLSHMSVDFPEMMAKIS 241
Db 832 IIACKRKNTSCSRFYQPTKLNSVQPARLHQFTDPLTLLSHMSVDFPEMMAKIS 891
Qy 242 VQVKLISKKUKPQIYHFO 260
Db 892 VQVKLISKKUKPQIYHFO 910

RESULT 5
B34721
androgen receptor B - human
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C; Accession: B34721
R; Govindan, M.V.

Mol. Endocrinol. 4, 417-427, 1990

Query Match 98.4%; Score 1349.5; DB 2; Length 919;
Best Local Similarity 99.6%; Pred. No. 2.6e-118;
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

A;Title: Specific region in hormone binding domain is essential for hormone binding and
A;reference number: A34721; MUID:90258935; PMID:2342476
A;accession: B34721
A;Molecule type: mRNA
A;Residues: 1-911 <GO2>
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: zinc finger
P;548-806/Domain: erba transforming protein homology <ERBA>
P;550-570/Region: zinc finger
P;586-610/Region: zinc finger

Query Match 95.3%; Score 1306; DB 2; Length 911;

Best Local Similarity 97.3%; Conservative 1; Pred. No. 3.1e-114; Mismatches 4; Indels 2; Gaps 2;

Qy 2 SHMIEGVGECOPTFLNLYEATBPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAK 61
Db 653 SH-IEGVECOPIFLNLYEATBPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAK 711

Qy 62 ALPGFERNLAVDQMDAVYQSYNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 121
Db 712 ALPGLRLHVDDOMAVTOYSNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 771

Qy 122 YSQCTVRMHLUSQEPGMQLITOPBFCLMKALLFSIPVDGKMQ-KFDPDELMVNTKELD 180
Db 772 YSQCVERNRHHSQEFGMQLITOPBFCLMKALLFSIPVDGKMQ-KFDPDELMVNTKELD 831

Qy 181 RIACKRKKNPSCSRRYQTLKUDSVQIARBLHPTFDLILKSMSVSDPEMMAI 240
Db 832 RIACKRKKNPSCSRRYQTLKUDSVQIARBLHPTFDLILKSMSVSDPEMMAI 891

Qy 241 SWQVPKILSGKVKPPIVHTQ 260
Db 892 SVQVPKILSGKVKPPIVHTQ 911

RESULT 6

151330 androgen receptor - common canary (fragment)
C;Species: Serinus canaria (common canary)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C;Accession: 151330
R;Naatik, K.I.; Clayton, D.P.
Endocrinology, 134, 640-647, 1994
A;Title: Seasonal and tissue-specific regulation of canary androgen receptor messenger
A;Reference number: 151330; MUID:94130808; PMID:8299561
A;Accession: 151330
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-344 <NAS>
A;Cross-references: GB:L025901; NID:9414733; PID:AAA17402.1; PID:9414734
A;Gene: AR
C;Genetics:
C;Keywords: zinc finger
P;1-251/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 88.8%; Score 1217; DB 2; Length 344;
Best Local Similarity 92.7%; Pred. No. 2e-106; Mismatches 5; Indels 0; Gaps 0;

Qy 5 IIGYECOPFLNLTEA1BPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAKLP 64
Db 100 IIGYECOPFLNLTEA1BPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAKLP 159

Qy 65 GRNLHYTDQMDAVYQSYNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 124
Db 160 GRNLHYTDQMDAVYQSYNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 219

Qy 125 CTYRHLHSQEFGLVQTPQEFCKMALKLIPPS1PVDGLKNOKLDFDLRMLNMVKELDRIA 184
Db 220 CTYRHLHSQEFGLVQTPQEFCKMALKLIPPS1PVDGLKNOKLDFDLRMLNMVKELDRIA 279

RESULT 7

JG0194 androgen receptor - Japanese eel

C;Species: Anguilla japonica (Japanese eel)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0194
R;Ito, T.; Ikeuchi, T.; Kobayashi, T.; Nagahama, Y.
Biochem. Biophys. Res. Commun., 254, 378-383, 1999

A;Title: Fish androgen receptor: cDNA cloning, steroid activation of transcription in tri
A;Reference number: JG0194; MUID:99119319; PMID:9918846
A;Accession: JG0194
A;Status: preliminary
A;Molecule type: mRNA

A;Superfamily: unassigned erba-related proteins; erba transforming protein homology
P;491-745/Domain: erba transforming protein homology <ERBA>

Query Match 65.6%; Score 900; DB 2; Length 848;

Best Local Similarity 68.1%; Pred. No. 3.7e-76; Mismatches 35; Indels 4; Gaps 2;

Qy 7 GIECOPFLNLTEA1BPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAKLP 66
Db 595 GIECOPFLNLTEA1BPGVVCAGHDNNQPSDFSAALISLMBELGEROLVHVKWAKLP 655

Qy 67 RNLAYDQMDAVYQSYNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 126
Db 656 RSLVYDQMDAVYQSYNGVGLMFAMGWSFTNVNSRMLYFADPLVNEYRMKSRM 715

Qy 127 RMRLHSQEFGLVQTPQEFCKMALKLIPPS1PVDGLKNOKLDFDLRMLNMVKELDRIA 186
Db 716 RMRLHSQEFGLVQTPQEFCKMALKLIPPS1PVDGLKNOKLDFDLRMLNMVKELDRIA 775

Qy 187 RKNITCSRRYQTLKUDSVQIARBLHPTFDLILKSMSVSDPEMMAI 244
Db 775 SK--SSCSRFOOTLRLUDSLOPVLKKLHFQTFDLYVQSONLSNOVCFEMISEISVH 833

Qy 245 PKLISGKVKPPIVFF 258
Db 834 PKLISGKVKPPIVFF 847

RESULT 8

A25923 progestrone receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 20-Aug-1999
C;Accession: A25923
R;Roozelt, H.; Anger, M.; Misrahi, M.; Giachon-Mantel, A.; Meriel, C.; Logeat, F.; Ben
Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986

A;Title: Cloning and sequence analysis of rabbit progestrone-receptor complementary DNA
A;Reference number: A25923; MUID:8707449; PMID:353016
A;Accession: A25923
A;Molecule type: mRNA
A;Residues: 1-930 <LO>
A;Cross-references: GB:NM14547; NID:9165631; PID:AAA131443.1; PID:9165632
C;Superfamily: progestrone receptor; erba transforming protein homology <ERBA>
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
P;1566-826/Domain: erba transforming protein homology <ERBA>
P;1566-588/Region: zinc finger
P;604-628/Region: zinc finger

Query Match 55.9%; Score 766; DB 2; Length 930;
Best Local Similarity 55.5%; Pred. No. 1.6e-63;

Matches	137;	Conservative	57;	Mismatches	53;	Indels	0;	Gaps	0;
Qy	12	PFLNLVLEAIEPGWVCAIGDNQDSFAALLSNEIGEROLVAKALPGRNHLV	71						
Db	682	PPLINLMSIEPDVIVAGHDNTKPDITSSLLTSINQGEROLLSVVKSKSLPGRNHL	741						
Qy	72	DDOMAVIQSYNGLMVAMGRSPFTNNSRMYFADLVNEYRMKSRSYQCVRMHL	131						
Db	742	DDOITLIOYSWSMISVFGLGNSYKRVSGOMYFAPDLVNEYRMKSRSYQCVRMHL	741						
Qy	132	SQRGWMQITPOEFLCMKALLFSIIPVGJLNQKEFDLERNAYIKELDRITACKRNPT	191						
Db	802	POFVFKLOQSOSERFLCMKVLLINTFLIGRSQSRPEMMSSYVILKIGRKGWV	861						
Qy	192	SCSRPYQLTKLSDVOPARELHOFTDILKSHMNSVDPPEMMMAISVQPKLISK	251						
Db	862	SSSQRPYQLTKLUDNLHDVKQHLYCLNTFQSRALSVFPEMSRVIAQPLKLAGM	921						
Qy	252	VKPIVHF	258						
Db	922	VKPLLFH	928						
RESULT 9									
ORHP									
progesterone receptor form B - human									
N;Alternate names:	hPR								
C;Species:	progestrone receptor form A								
C;Date:	30-Jun-1987	#sequence revision 18-Nov-1994	#text_change 22-Jun-1999						
C;Accession:	SG9971; S12464; R03245								
R;Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gromemeyer, H.; Chamson, E									
EMBO J. 9, 1603-1614, 1990									
A;Title:	Two distinct estrogen-regulated promoters generate transcripts encoding the two								
A;Reference number:	S09971; MUID:90228361; PMID:2328727								
A;Accession:	S09971								
A;Molecule type:	mRNA								
A;Residues:	1-333 <XAS>								
A;Cross-references:	EMBL:X51730								
R;Kaatze, P.									
submitted to the EMBL Data Library, February 1990									
A;Reference number:	S12464								
A;Accession:	S12464								
A;Molecule type:	mRNA								
A;Cross-references:	EMBL:X51730; NID:935551; PIDN:CAA36018.1; PID:935552								
R;Misrahi, M.; Atger, M.; D'Auriol, L.; Loosfelt, H.; Meriel, C.; Fridlansky, F.; Guiot, E									
Biochem. Biophys. Res. Commun. 143, 740-748, 1987									
A;Title:	Complete amino acid sequence of the human progesterone receptor deduced from cDNA								
A;Reference number:	A03245; MUID:87184565; PMID:3551956								
A;Accession:	A03245								
A;Molecule type:	mRNA								
A;Residues:	1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <NIS>								
A;Cross-references:	GB:ML1516; NID:9189934; PIDN:AAA60081.1; PID:9189935								
A;Genes:	GB:PGR								
A;Cross-references:	GDB:119493; OMIM:264080								
A;Map position:	11q22.1-11q22.3								
C;Superfamily:	Progesterone receptor; erbA transforming protein homology								
C;Keywords:	alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormone								
P;1-933/Products:	Progesterone receptor form B #status predicted <MA2>								
P;165-933/Product:	Progesterone receptor form A #status predicted <MA2>								
P;565-829/Domain:	erbA transforming protein homology <ERBA>								
P;567-587/Region:	zinc finger CCCC motif								
P;603-627/Region:	zinc finger CCCC motif								
P;681-933/Domain:	steroid binding #status predicted <STR>								
P;411/Binding Site:	steroid (Tyr) (covalent) #status predicted								
P;227, 232, 552, 793/Binding site:	phosphate (Ser) (covalent) #status predicted								
P;329, 374, 601/Binding site:	phosphate (Tyr) (covalent) #status predicted								
Query Match	55.8%; Score 765; DB 1; Length 933;								
Best Local Similarity	55.5%; Pred. No. 246-63;								
Matches	137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;								
RESULT 9									
Qy	12	PFLNLVLEAIEPGWVCAIGDNQDSFAALLSNEIGEROLVAKALPGRNHLV	71						
Db	685	PPLINLMSIEPDVIVAGHDNTKPDITSSLLTSINQGEROLLSVVKSKSLPGRNHL	741						
Qy	72	DDOMAVIQSYNGLMVAMGRSPFTNNSRMYFADLVNEYRMKSRSYQCVRMHL	131						
Db	742	DDOITLIOYSWSMISVFGLGNSYKRVSGOMYFAPDLVNEYRMKSRSYQCVRMHL	741						
Qy	132	SQRGWMQITPOEFLCMKALLFSIIPVGJLNQKEFDLERNAYIKELDRITACKRNPT	191						
Db	802	POFVFKLOQSOSERFLCMKVLLINTFLIGRSQSRPEMMSSYVILKIGRKGWV	861						
Qy	192	SCSRPYQLTKLSDVOPARELHOFTDILKSHMNSVDPPEMMMAISVQPKLISK	251						
Db	862	SSSQRPYQLTKLUDNLHDVKQHLYCLNTFQSRALSVFPEMSRVIAQPLKLAGM	921						
Qy	252	VKPIVHF	258						
Db	922	VKPLLFH	928						
RESULT 10									
Qy	153280								
ORHP									
progesterone receptor B form - rat									
C;Species:	Rattus norvegicus (Norway rat)								
C;Date:	02-Aug-1996	#sequence revision 02-Aug-1996	#text_change 20-Aug-1999						
C;Accession:	I53280; B13733; A49374; A23733								
R;Park-Sarge, O.K.; Mayo, K.B.									
Endocrinology 134, 709-718, 1994									
A;Title:	Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine monophosphate								
A;Reference number:	153280; MUID:94130817; PMID:8299566								
A;Accession:	I53280								
A;Status:	preliminary								
A;Molecule type:	mRNA								
A;Residues:	1-923 <PAR1>								
R; Park, O.K.; Mayo, K.B.									
Mol. Endocrinol. 5, 967-978, 1991									
A;Cross-references:	GB:S64044								
R;Kraus, W.L.; Montano, M.M.; Katzenellenbogen, B.S.									
Mol. Endocrinol. 7, 1603-1616, 1993									
A;Title:	Cloning of the rat progesterone receptor gene 5'-region and identification of transcriptional elements								
A;Reference number:	A49374; MUID:94195318; PMID:8145766								
A;Accession:	A49374								
A;Status:	preliminary								
A;Molecule type:	DNA								
A;Residues:	1-16 <XRA>								
A;Cross-references:	GB:S69361; NID:9546178								
C;Superfamily:	Progesterone receptor; erbA transforming protein homology								
C;Keywords:	DNA binding; nucleus; steroid hormone receptor; zinc finger								
P;55-819/Domain:	erbA transforming protein homology <ERBA>								
P;557-577/Region:	zinc finger								
Query Match 55.4%; Score 759; DB 2; Length 923;									
Best Local Similarity 55.5%; Pred. No. 7.1.e-63;									
Matches 137; Conservative 55; Mismatches 55; Indels 0; Gaps 0;									
Qy	12	PFLNLVLEAIEPGWVCAIGDNQDSFAALLSNEIGEROLVAKALPGRNHLV	71						
Db	675	PPLINLMSIEPDVIVAGHDNTKPDITSSLLTSINQGEROLLSVVKSKSLPGRNHL	734						
Qy	72	DDOMAVIQSYNGLMVAMGRSPFTNNSRMYFADLVNEYRMKSRSYQCVRMHL	131						
Db	735	DDOITLIOYSWSMISVFGLGNSYKRVSGOMYFAPDLINEORMKSLPGRNHL	794						

QY 72 DDOMAVIQISWMGLMPANGWRSFTIVNSRMLYFADLVENRYKMSRMYSQVRAHL 131
 Db 590 DDQMTLLOQSWMFLMAPLGWRSYROSSAMICRAPPDLINERQMTLPCMYDQCKHMLV 649
 QY 132 SQEFQWLQLTPOEFLCMAKALLFLSTIPVDGILKRNQKFDELMNYKEDRICKRIFT 191
 Db 650 SSELRLQLQSYEYLQMTLILSVPKDGIKSQSLFDEIRMVYKLKGAIVERGENSS 709
 QY 192 SCSPRQLQTLKLSVQPIARBLHQTDFDLIKSHMSVSDPPEMAETISVOVRKLSGK 251
 Db 710 QNWORKYOLTKLDSRHEVVNLNLCFQFDKTM-SIPEPMABITNQIKRISGN 768
 QY 252 VPKIYFH 258
 Db 769 :|||:
 Db 769 IKKULFH 775

RESULT 15

A41401
 mineralocorticoid receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-sep-1999
 C;Accession: A41401
 R;Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
 Mol. Endocrinol. 3, 1877-1885, 1989
 A;Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA for
 A;Reference number: A41401; MUID:90114194; PMID:2558305
 A;Accession: A41401
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-981 <PAT>
 A;Cross-references: GB:M36074; NID:9205340; PID:AAA41583.1; PID:g205341
 C;superfamily: unassigned
 C;Keywords: DNA binding; transcription regulation; zinc finger
 F;602-877/Domain: erba transforming protein homology <ERBA>
 F;624-624/Region: zinc finger
 F;640-664/Region: zinc finger

Query Match Local Similarity 48.3%; Score 662; DB 2; Length 981;
 Matches 128; Conservative 47; Mismatches 64; Indels 6; Gaps 2;
 Qy 17 VLEATERPVGWCGHDNNOPDSFAAFLSSNLNEGEROLVHVVKWAKALPGFRNLHVDDOMA 76
 Db 738 ILENIEPTEPVYAGYDONSKEPDTAESLSTLNRAKOMIQVVKWAKVLPGEFKNLPLEDQT 797
 Qy 77 VIQYSUNGIAFMGRSPINVRNSRMLYFADLVENRYKMSRMYSQCTMRHHSQEG 136
 Db 798 LIQYSWNCLSSPALSWSYKTNINSOLYFAPDLVENEKEMOISAMYBLCOGMROTSIQLFV 857
 Qy 137 WQQTQBFLLCKALMPLSIIIVDGKKNQKEFDELRYNKEDRITACKKNPTSCS-- 194
 Db 858 RLQLTPEYKSYMKVLLSITWPDKGKSKQAFEEEMTYKELKMT--KCPNSGQS 914
 Qy 195 -RFYQYTKLSDVQPIARBLHQTDFDLIKSHMSVSDPPEMAETISVOVKLGSKVK 253
 Db 915 WQRFYQYOLTKLDSRHEVVNLNLCFQFDKTM-SIPEPMABITNQIKRISGN 974
 Qy 254 PIYFH 258
 Db 975 PIYFH 979

Search completed: October 9, 2003, 11:43:05
 Job time : 20 secs

Db 125 YSOQVVRMHLSSQFGLWQITPQEFLKMLLFSIIPVPGIKNQPFDELRYNIKELDR 184 ; SEQ ID NO: 2
 Qy 182 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 241 ; LENGTH: 907
 Db 185 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 244 ; TYPE: PRT
 Qy 242 VQVPKILSGKVKP1YHTQ 260 ; ORGANISM: Canine
 Db 245 VQVPKILSGKVKP1YHTQ 263 ; US-10-008-739A-2

RESULT 2
 US-09-997-267-2
 Sequence 2, Application US/09997267
 Patent No. US20020165381A1
 GENERAL INFORMATION:
 APPLICANT: AHNRENS-FATH, ISABELLE
 APPLICANT: HAENDLER, BERNARD
 TITLE OF INVENTION: HUMAN ANDROGEN RECEPTOR VARIANTS
 FILE REFERENCE: SCH-1793
 CURRENT APPLICATION NUMBER: US/09/997,267
 CURRENT FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 60/355,078
 PRIOR FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 388
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-997-267-2.

Query Match 98.4%; Score 1349.5; DB 10; Length 388;
 Best Local Similarity 99.6%; Pred. No. 2e-142; 0; Mismatches 0; Indels 1; Gaps 1;
 Matches 258; Conservative 0; MisMatches 0; Indels 1; Gaps 1;

Qy 2 SHMIEGTYECQPIFLNVLRAIEPGVUCAGHDNNQDSPIALISSNLIGEROLHVNWKAK 61 ;
 Db 131 SH-1EGYECQPIFLNVLRAIEPGVUCAGHDNNQDSPIALISSNLIGEROLHVNWKAK 189 ;
 Qy 62 ALPGFRNLHDDQMAVQIWSWGMGLAVFAMGWRSPFTNNSRMLYAPDLVNEYRMHKSRM 121 ;
 Db 190 ALPERNLADDDQMAVQIWSWGMGLAVFAMGWRSPFTNNSRMLYAPDLVNEYRMHKSRM 249 ;
 Qy 122 YSOQVVRMHLSSQFGLWQITPQEFLKMLLFSIIPVPGIKNQPFDELRYNIKELDR 181 ;
 Db 250 YSOQVVRMHLSSQFGLWQITPQEFLKMLLFSIIPVPGIKNQPFDELRYNIKELDR 309 ;
 Qy 182 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 241 ;
 Db 310 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 369 ;
 Qy 242 VQVPKILSGKVKP1YHTQ 260 ;
 Db 370 VQVPKILSGKVKP1YHTQ 388 ;
 Db 650 SH-1EGYECQPIFLNVLRAIEPGVUCAGHDNNQDSPIALISSNLIGEROLHVNWKAK 708 ;
 Qy 62 ALPGFRNLHDDQMAVQIWSWGMGLAVFAMGWRSPFTNNSRMLYAPDLVNEYRMHKSRM 121 ;
 Db 709 ALPGFRNLHDDQMAVQIWSWGMGLAVFAMGWRSPFTNNSRMLYAPDLVNEYRMHKSRM 768 ;
 Qy 122 YSOQVVRMHLSSQFGLWQITPQEFLKMLLFSIIPVPGIKNQPFDELRYNIKELDR 181 ;
 Db 769 YSOQVVRMHLSSQFGLWQITPQEFLKMLLFSIIPVPGIKNQPFDELRYNIKELDR 828 ;
 Qy 182 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 241 ;
 Db 829 IACKRKNPISCSRFRYQTLKLSVQPIARBLHQFTDILKSHMSVDPEMMARIS 888 ;
 Qy 242 VQVPKILSGKVKP1YHTQ 260 ;
 Db 889 VQVPKILSGKVKP1YHTQ 907 ;

RESULT 4
 US-10-205-823-36
 Sequence 36, Application US/10205823
 Publication No. US20030108963A1
 GENERAL INFORMATION:
 APPLICANT: Schlegel, Robert
 APPLICANT: Monahan, John E.
 APPLICANT: Endege, Wilson O.
 APPLICANT: Gammavaru, Manjula
 APPLICANT: Gorbatcheva, Bella
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Wonsley, Angela M.
 APPLICANT: Glatt, Karen
 APPLICANT: Zhao, Xumei
 APPLICANT: Anderson, Dustin
 TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
 FILE REFERENCE: MRI-044
 CURRENT APPLICATION NUMBER: US/10/205,823
 CURRENT FILING DATE: 2002-07-25,
 PRIOR APPLICATION NUMBER: 60/307,982
 PRIOR FILING DATE: 2001-07-25
 PRIOR APPLICATION NUMBER: 60/314,356
 PRIOR FILING DATE: 2001-08-22
 PRIOR APPLICATION NUMBER: 60/325,020
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 60/341,746
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: 60/362,158
 PRIOR FILING DATE: 2002-03-05
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 36
 LENGTH: 919
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-205-823-36

Query Match 98.4%; Score 1349.5; DB 15; Length 919;
 Best Local Similarity 99.4%; Pred. No. 7e-142;
 FILE REFERENCE: PCT0893AGER
 CURRENT APPLICATION NUMBER: US/10/008,739A
 CURRENT FILING DATE: 2002-04-15
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn version 3.1

Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 SHMIEGYCOPIFTNLVRAEPIGVCAHGDNQDSFAALLSINELGEROLVHVVKWAK 61
Db 662 SH-IEGYBCOPIFTNLVLAEREPGVCAHGDNQDSFAALLSINELGEROLVHVVKWAK 720

Qy 62 ALPGFRNLHDDOMAVIOTSGWGLMVFMGWSFTNNSRMYFADLVNEYRHMHSRM 121
Db 721 ALPGFRNLHDDOMAVIOTSGWGLMVFMGWSFTNNSRMYFADLVNEYRHMHSRM 121

Qy 122 YSOCVRMRLSQEFGWLOITPQBLCMKALLFSIIPDGLKNOKEFDLRLMNTKEDR 181
Db 781 YSOCVRMRLSQEFGWLOITPQBLCMKALLFSIIPDGLKNOKEFDLRLMNTKEDR 840

Qy 182 TIACKERKNPSSRSRPFQTLKLSVQPTARBLQHPTDFDLKSHMSVDFPEMAETIS 241
Db 841 TIACKERKNPSSRSRPFQTLKLSVQPTARBLQHPTDFDLKSHMSVDFPEMAETIS 900

Qy 242 WVKPLSGKVKPFIYHTQ 260
Db 901 VVKPLSGKVKPFIYHTQ 919

RESULT 5
US-09-885-827-1

; Sequence 1, Application US/09885827

; Patent No. US20020173445A1

; GENERAL INFORMATION:

; APPLICANT: Salvati, Mark

; APPLICANT: Attar, Ricardo M

; APPLICANT: Kryteck Jr., Stanley R

; APPLICANT: Gottardis, Marco M

; CURRENT APPLICATION NUMBER: US/09/885,827

; CURRENT FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: 60/284,438

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/214,392

; PRIOR FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS.: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 246

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-997-267-4

RESULT 6
US-09-997-267-4

; Sequence 4, Application US/09997267

; Patent No. US20020165381A1

; GENERAL INFORMATION:

; APPLICANT: AHRENS-PATH, ISABELLE

; APPLICANT: HAENDLER, BERNARD

; TITLE OF INVENTION: HUMAN ANDROGEN RECEPTOR VARIANTS

; FILE REFERENCE: SCH-1793

; CURRENT APPLICATION NUMBER: US/09/997,267

; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/255,078

; PRIOR FILING DATE: 2000-12-14

; NUMBER OF SEQ ID NOS.: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 294

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-997-267-4

Query Match 59.3%; Score 813.5; DB 10; Length 294;
Best Local Similarity 99.4%; Pred. No. 1.5e-82; Mismatches 0; Indels 1; Gaps 1;

Matches 154; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 SHMIEGYCOPIFTNLVRAEPIGVCAHGDNQDSFAALLSINELGEROLVHVVKWAK 61
Db 131 SH-IEGYBCOPIFTNLVLAEREPGVCAHGDNQDSFAALLSINELGEROLVHVVKWAK 189

Qy 62 ALPGFRNLHDDOMAVIOTSGWGLMVFMGWSFTNNSRMYFADLVNEYRHMHSRM 121
Db 190 ALPGFRNLHDDOMAVIOTSGWGLMVFMGWSFTNNSRMYFADLVNEYRHMHSRM 249

Qy 122 YSOCVRMRLSQEFGWLOITPQBLCMKALLFSI 156
Db 250 YSOCVRMRLSQEFGWLOITPQBLCMKALLFSI 284

RESULT 7
US-10-220-981-3

; Sequence 3, Application US/10220981

; Publication No. US20030167999A1

; GENERAL INFORMATION:

; APPLICANT: Schering AG

; APPLICANT: Donner, Peter

; APPLICANT: Eigner, Ursula

; APPLICANT: Carrondo, Maria A

; APPLICANT: Matias, Pedro M

; TITLE OF INVENTION: Crystal

; FILE REFERENCE: P008463M0 CTH

; CURRENT APPLICATION NUMBER: US/10/220,981

; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: GB 0005689.5

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS.: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 258

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-220-981-3

Query Match 55.8%; Score 765; DB 12; Length 258;
Best Local Similarity 55.5%; Pred. No. 3.3e-77; Mismatches 57; Indels 0; Gaps 0;

Matches 137; Conservative 57; Mismatches 53;

Qy 12 PFLNLYTLEAPIRGVCAHGDNQDSFAALLSINELGEROLVHVVKWAKALPGFRNLH 71
Db 121 QFPGWMLQITPBLCMKALLFSIIPDGLKNOKEFDLRLMNTKEDR1ACAAAAS 180

Qy 193 CSRRPVQLTKLDSVQPIARELHQFFDLIKSHMSVDFPEMAETISVVKPLSGKV 252
Db 181 CSRRPVQLTKLDSVQPIARELHQFFDLIKSHMSVDFPEMAETISVVKPLSGKV 240

Qy 253 KPYIFH 258
Db 241 KPYIFH 246

Qy 72 DDONAVTOSWMGLMVFMGWSFTNNSRMYFADLVNEYRHMHSRMYSOCVRMHL 131

RESULT 11
US-09-905-176-11
; Sequence 11, Application US/0905176
; Patent No. US20020150906A1
; GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: Debe, Derek A.
TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM FILE REFERENCE: 265/297
CURRENT APPLICATION NUMBER: US/09/905,176
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/218,016
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-176-11

Query Match Best Local Similarity 48.3%; Score 662.5; DB 15; Length 777;
Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;
Best Local Similarity 50.6%; Pred. No. 4.9e-65; DB 15; Length 777;
Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

Qy 28 AGHDNNQPSKAALLSSLINEGEROLVHVVKAKALPGRFLNQIHDQMAVIVQYSWMLMV 87
Db 1 AGHDNNQPSKAALLSSLINEGEROLVHVVKAKALPGRFLNQIHDQMAVIVQYSWMLMV 60

Qy 88 PAMGWSFTNVNSRMVYAPDILVFNRYRMRHKSRSVCRHRHSQCVRMHLQITPROFLC 147
Db 61 FGGLGRSYKHSQMLYFADPLILNORMKESFSFISLCLTWQIQFBVFLQVSOREFLC 120

Qy 148 MKALALFSLIPFDGLKNOKEFDELRYNYIKELDRITACKRNQPNCSRRYQLOKLDSV 207
Db 121 MKVLLINTIPLEGILRSOTOPERMSSYIRLKLKGRLQKGVSSQRQLQTKLNL 180

Qy 208 QPIARBLHQTFPDLLIKSHMSVDPREMMABIS 241
Db 181 HDLVQKQHLCINTPQSRALSVVERPEMMBSVIA 214

RESULT 12
US-10-153-668-226
; Sequence 226, Application US/10153668
; Publication No. US2003009216A1
; GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: START Activating Gene FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 226

Query Match Best Local Similarity 45.6%; Score 662; DB 15; Length 689;
Matches 121; Conservative 59; Mismatches 75; Indels 0; Gaps 0;
Best Local Similarity 47.5%; Pred. No. 4.7e-65; DB 15; Length 689;
Matches 121; Conservative 59; Mismatches 75; Indels 0; Gaps 0;

Qy 4 MERGYSCQPIEFTNVNLAEPSGVCAHHNNQPSKAALLSSLINEGEROLVHVVKAKALPGRFLNQIHDQMAVIVQYSWMLMV 63
Db 433 MYRLQFTPQQLSILENTIEPERIVVSYDATOPETPHLNSLNGCEROLVHVVKAKALPGRFLNQIHDQMAVIVQYSWMLMV 63

Qy 64 PGRFLNQIHDQMAVIVQYSWMLMVFAMGWSFTNVNSRMVYAPDILVFNRYRMRHKSRSVCRHRHSQCVRMHL 123
Db 493 PGFRSLHINDONTLQYSWMLMVLSGLMSFQNTREPFYFADPLILNORMKESFSFISLCLTWQIQFBVFLQVSOREFLC 552

Qy 124 QCVRMHLHQTFPDLLIKSHMSVDPREMMABIS 183
Db 553 LCMAMQOLIPQAEDNLQVTKESFCLCKMLLJNTIPLEGILRSOTOPERMSSYIRLKLKGRLQKGVSSQRQLQTKLNL 612

Qy 184 ACKRKPTSCSERFVQTLKLDVSGPTARLHQTFPDLLIKSHMSVDPREMMABIS 243

RESULT 14
 US-10-001-486B-2
 ; Sequence 2, Application US/10001486B
 ; Publication No. US20030082642A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America
 ; as represented by the Secretary
 ; Department of Health and Human Services
 ; Washington, D.C.
 ; Htun, Ph.D., Han
 ; Hager, Ph.D., Gordon L.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NEEDLE & Rosenberg
 ; STREET: 127 Peachtree Street, Suite 1200
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/001-486B
 ; FILING DATE: 15-NO-001486B-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/008,373
 ; FILING DATE: 08 Dec 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Selby, Elizabeth
 ; REGISTRATION NUMBER: 38288
 ; REFERENCE/DOCKET NUMBER: 14014.0183
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-688-0770
 ; TELEFAX: 404-688-9880
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1070 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-001-486B-2

Query Match 46.6%; Score 639.5; DB 15; Length 1070;
 Best Local Similarity 49.4%; Pred. No. 3e-62; Mismatches 122; Conservative 48; Gaps 1; Indels 1;

Qy 12 PIPLVLAERLPPGVVAGHNNNQPSFAALISNLGERLVHVKAKALPERMIAV 71
 Db 823 PTVLVSLLEVTPRPEVLYAGYDSSVPDSAWRTMTLNGGGRTAAVWKAKILGRLHL 882

Qy 72 DDQMAVQSYWGMVAMPGRSFTVNSRMVYFADLVNEVRMHSRMSQCVRMRHL 131
 Db 883 DDQMLQSYWGMVAMPGRSYFQSGNLLPAPLILNEQRSLPMDQKHLFV 942

Qy 132 SOERGMQITPQFLCKMALLFSITPVDGKQKFDRBRMYTKELDRITACKRNP 191
 Db 943 SSELQLQSVSYEYLCKMLLSSVKEGLKSOLFDEIRTYKELGKALVKREGNS 216

Qy 192 SCRRFVQTKLUDSVPIARELHQFDLJSHMSVDFEMMABIIISVOPKLISK 251
 Db 217 QNMRFGITKLDMSHEVENILTYCQTFDLKTW-SIEPEMLABITNOIPKSN 275

Qy 252 VKGIVFH 288
 Db 276 IKCLIFH 282

Search completed: October 9, 2003, 11:43:39
 Job time : 28 secs

RESULT 15
 US-09-683-450-20
 ; Sequence 20, Application US/09853450
 ; Publication No. US20020194645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Palaz, Soraya
 ; APPLICANT: Ditta, Gary
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
 ; FILE REFERENCE: 19452A-002400US
 ; CURRENT APPLICATION NUMBER: US/09/683,450
 ; CURRENT FILING DATE: 2001-05-09
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; OTHER INFORMATION: rat glucocorticoid receptor ligand binding domain
 ; US-09-683-450-20

Query Match 46.0%; Score 630.5; DB 10; Length 284;
 Best Local Similarity 49.0%; Pred. No. 4.4e-62; Mismatches 121; Conservative 48; Gaps 1; Indels 1;

Qy 12 PIPLVLAERLPPGVVAGHNNNQPSFAALISNLGERLVHVKAKALPERMIAV 71
 Db 37 PTVLVSLLEVTPRPEVLYAGYDSSVPDSAWRTMTLNGGGRTAAVWKAKILGRLHL 96

Qy 72 DDQMAVQSYWGMVAMPGRSFTVNSRMVYFADLVNEVRMHSRMSQCVRMRHL 131
 Db 97 DDQMLQSYWGMVAMPGRSYFQSGNLLPAPLILNEQRSLPMDQKHLFV 156

Qy 132 SOERGMQITPQFLCKMALLFSITPVDGKQKFDRBRMYTKELDRITACKRNP 191
 Db 157 SSELQLQSVSYEYLCKMLLSSVKEGLKSOLFDEIRTYKELGKALVKREGNS 216

Qy 192 SCRRFVQTKLUDSVPIARELHQFDLJSHMSVDFEMMABIIISVOPKLISK 251
 Db 217 QNMRFGITKLDMSHEVENILTYCQTFDLKTW-SIEPEMLABITNOIPKSN 275

Qy 252 VKGIVFH 288
 Db 276 IKCLIFH 282

Db 1003 QNMRFGITKLDMSHEVENILTYCQTFDLKTW-SIEPEMLABITNOIPKSN 1061
 Qy 252 VKGIVFH 258
 Db 1062 IKCLIFH 1068

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 9, 2003, 11:39:53 ; Search time 19 Seconds

Sequence: 1 GHSMIBGYECQPIFLNLEA.....SNQVPKILSGVKPFIYFHQ 260

Scoring table: BLOSUM62

Searched: Gapext 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ISSUED_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1349.5	98.4	452	3 US-08-764-870-16 Sequence 16, Appl
2	1349.5	98.4	452	3 US-08-764-870-16 Sequence 16, Appl
3	1349.5	98.4	918	3 US-09-041-886-11 Sequence 11, Appl
4	766	55.9	363	6 5223606-5 Patent No. 5223606
5	765	55.8	933	3 US-08-764-870-14 Sequence 14, Appl
6	765	55.8	933	3 US-08-764-870-14 Sequence 14, Appl
7	665	48.5	984	3 US-08-764-870-15 Sequence 15, Appl
8	665	48.5	984	3 US-08-764-870-15 Sequence 15, Appl
9	665.5	48.3	777	3 US-08-764-870-13 Sequence 13, Appl
10	662.5	48.3	777	3 US-08-764-870-13 Sequence 13, Appl
11	644.5	47.0	534	3 US-08-875-223-8 Sequence 8, Appl
12	633.5	46.6	1070	4 US-09-091-0424-2 Sequence 2, Appl
13	638.5	46.6	284	2 US-09-593-214A-24 Sequence 24, Appl
14	638.5	46.6	284	3 US-09-149-976-24 Sequence 24, Appl
15	630.5	46.6	1	US-07-716-827C-5 Sequence 5, Appl
16	630.5	46.0	284	3 US-08-650-188-20 Sequence 20, Appl
17	630.5	46.0	284	3 US-08-655-227-20 Sequence 20, Appl
18	630.5	46.0	284	3 US-08-655-241-20 Sequence 20, Appl
19	630.5	46.0	284	4 US-09-398-326-20 Sequence 20, Appl
20	626	45.7	356	6 5223606-7 Patent No. 5223606
21	224	16.3	60	5 PCT-US94-14074-1 Sequence 1, Appl
22	211.5	15.4	284	2 US-08-836-620A-16 Sequence 16, Appl
23	209	15.2	450	4 US-08-839-839-4 Sequence 4, Appl
24	207.5	15.1	595	3 US-08-763-870-12 Sequence 12, Appl
25	207.5	15.1	595	3 US-08-980-115-12 Sequence 12, Appl
26	206.5	15.1	484	2 US-08-833-620A-13 Sequence 13, Appl
27	206.5	15.1	485	2 US-08-836-620A-13 Sequence 12, Appl

ALIGNMENTS

RESULT 1	US-08-764-870-16
Sequence 16, Application US/08764870	PATENT NO. 6246946
GENERAL INFORMATION:	
APPLICANT: Scanlan, Thomas S	APPLICANT: Baxter, John D
APPLICANT: Fleterick, Robert J	APPLICANT: Wagner, Richard L
APPLICANT: Kushner, Peter J	APPLICANT: Apriletti, James W
APPLICANT: West, Brian	APPLICANT: Nuclear Receptor Ligands and I
NUMBER OF SEQUENCES: 16	TITLE OF INVENTION: Binding Domains
CORRESPONDENCE ADDRESS:	ADDRESS: Cooley Godward
STREET: Five Palo Alto Square,	3000 El Camino F
CITY: Palo Alto	STATE: CA
ZIP: 94306	ZIP: 94306
COUNTRY: USA	COUNTRY: USA
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #11.0, Version #1.30	SOFTWARE: Patentn Release #11.0, Version #1.30
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-764,870	APPLICATION NUMBER: US/08-764,870
FILING DATE: 13-DEC-1996	FILING DATE: 13-DEC-1996
CLASSIFICATION: 530	CLASSIFICATION: 530
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540	APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995	FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606	APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995	FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N	NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966	REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UAL-246/01US	REFERENCE/DOCKET NUMBER: UAL-246/01US
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 843-5000	TELEPHONE: (650) 843-5000
INFORMATION FOR SEQ ID NO: 16:	INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids	LENGTH: 452 amino acids
TYPE: amino acid	TYPE: amino acid

Sequence 2, Appli
Sequence 2, Appli
Sequence 17, Appli
Sequence 35, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 3, Appli
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Sequence 1, Appli
Sequence 14, Appli
Sequence 5, Appli
Sequence 1, Appli

;

;

STRANDBIASNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

;

US-08-764-870-16

Query Match 98.4%; Score 1349.5; DB 3; Length 452;
Best Local Similarity 99.6%; Pred. No. 9.1e-147; Mismatches 0; Indels 1; Gaps 1;
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMTEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 61

Db 195 SH-IEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 253

QY 62 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 121

Db 254 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 313

QY 122 YSQCVRMHLSQFGMLQITPQBLKMKLILFSIIPVDGLKKNQKFPELMNYIKELDR 181

Db 314 YSQCVRMHLSQFGMLQITPQBLKMKLILFSIIPVDGLKKNQKFPELMNYIKELDR 373

QY 182 IACKRKNTCSRRPYQIQLKLDSDVQPTARBLHQPTPLDLIKSHMVSDFPENNMAETIS 241

Db 374 IACKRKNTCSRRPYQIQLKLDSDVQPTARBLHQPTPLDLIKSHMVSDFPENNMAETIS 433

QY 242 VQVPKILSGKVKKPKIYHTQ 260

Db 434 VQVPKILSGKVKKPKIYHTQ 452

;

RESULT 2

US-08-980-115-16

;

Sequence 16, Application US/08980115

;

Patent No. 6266622

;

GENERAL INFORMATION:

;

APPLICANT: Scanlan, Thomas S.

;

APPLICANT: Baxter, John D.

;

APPLICANT: Fetterick, Robert J.

;

APPLICANT: Wagner, Richard L.

;

APPLICANT: Kushner, Peter J.

;

APPLICANT: Apriletti, James W.

;

APPLICANT: West, Brian L.

;

APPLICANT: Shiu, Andrew K.

;

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS

;

FILE REFERENCE: UCAL-246-02US

;

CURRENT APPLICATION NUMBER: US/08/980,115

;

EARLIER APPLICATION NUMBER: 08/764,870

;

EARLIER FILING DATE: 1995-12-13

;

EARLIER APPLICATION NUMBER: 60/008,606

;

EARLIER FILING DATE: 1995-12-14

;

EARLIER APPLICATION NUMBER: 60/008,543

;

EARLIER FILING DATE: 1995-12-13

;

EARLIER APPLICATION NUMBER: 60/008,540

;

NUMBER OF SEQ ID NOs: 17

;

SOFTWARE: PatentIn Ver. 2.0

;

SRO ID NO 16 LENGTH: 452

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

FEATURE: DOMAIN

;

NAME/KEY: (184) . . . (437)

;

LOCATION: minimal ligand binding domain

;

US-08-980-115-16

Query Match 98.4%; Score 1349.5; DB 3; Length 452;
Best Local Similarity 99.6%; Pred. No. 9.1e-147; Mismatches 0; Indels 1; Gaps 1;
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMTEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 61

Db 661 SH-IEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 719

QY 62 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 121

Db 720 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 779

QY 122 YSQCVRMHLSQFGMLQITPQBLKMKLILFSIIPVDGLKKNQKFPELMNYIKELDR 181

;

RESULT 3

US-09-041-886-11

;

Sequence 11, Application US/09041886

;

Patent No. 6235872

;

GENERAL INFORMATION:

;

APPLICANT: Bredeben, Dale E.

;

APPLICANT: Rabizadeh, Sharroz

;

TITLE OF INVENTION: Protoprotic Peptides, Dependence
TITLE OF INVENTION: Protoprotic Peptides, Dependence
NUMBER OF SEQUENCES: 72

;

CORRESPONDENCE ADDRESS:

;

ADDRESSEE: Campbell & Flores LLP

;

STREET: 4370 La Jolla Village Drive, Suite 700

;

CITY: San Diego

;

STATE: California

;

COUNTRY: United States

;

ZIP: 92122

;

COMPUTER READABLE FORM:

;

MEDIUM/TYPE: Floppy disk

;

COMPUTER: IBM PC compatible

;

OPERATING SYSTEM: PC-DOS/MS-DOS

;

REFERENCE/DOCKET NUMBER: P-LJ 2626

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/09/041,886

;

FILING DATE:

;

CLASSIFICATION:

;

ATTORNEY/AGENT INFORMATION:

;

NAME: Campbell, Kathryn A.

;

REGISTRATION NUMBER: 31,815

;

REFERENCE/DOCKET NUMBER: P-LJ 2626

;

TELECOMMUNICATION INFORMATION:

;

TELEPHONE: (619) 535-9001

;

TELEFAX: (619) 535-9499

;

INFORMATION FOR SEQ ID NO: 11:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 918 amino acids

;

TYPE: amino acid

;

TOPOLOGY: linear

;

MOLECULE TYPE: protein

;

US-09-041-886-11

;

Query Match 98.4%; Score 1349.5; DB 3; Length 918;
Best Local Similarity 99.6%; Pred. No. 2.6e-146; Mismatches 0; Indels 1; Gaps 1;
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMTEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 61

Db 661 SH-IEGYECQPIFLNLVLAIEPGVVCAGHDNNQPSFAALLSSNLNEGERQLHVVKWAK 719

QY 62 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 121

Db 720 ALPGFRNLHVDDOMAVIQYSWMLVFMGMRSPFTVNSRMLYFAPDLYNEYRMKSRM 779

QY 122 YSQCVRMHLSQFGMLQITPQBLKMKLILFSIIPVDGLKKNQKFPELMNYIKELDR 181

; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: UCAL-246/02US
; CURRENT APPLICATION NUMBER: US/08/980,115
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 08/764,870
; EARLIER FILING DATE: 1995-12-13
; EARLIER FILING DATE: 1995-12-14
; EARLIER APPLICATION NUMBER: 60/008,543
; EARLIER FILING DATE: 1995-12-13
; EARLIER FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (659)..(918)
; OTHER INFORMATION: minimal ligand binding domain
; US-08-980-115-14

Query Match 55.8%; Score 765; DB 3; Length 933;
Best Local Similarity 55.5%; Pred. No. 5_6a-79; Mismatches 53; Indels 0; Gaps 0;
Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;

Oy 12 PIFAVNLVATEIPGTVCAHHDDNNOPDSFAALLSSNLNGERQHVVKAALPGPFRMLV 71
Db 685 PPLINLMSIEPDVYAGHDNTRKDIDSSSLTSNLNGEROLLSSVRKNSRPGFRNLH 744
Oy 72 DPDQAVIQYSWGMMPAMGRSRFTNVNSRMLYFADLVNEYRMEKRSRMSQCVRMHSQBG 131
Db 745 DDOITLQTSWMSLMVPGLGWSRYSKHSVQSMYAPPDLINTEONKRSKPSYSLCTM01 804

Oy 132 S0BGMQLQTPIBLCKMALLSFILPVGLKRNKFPLBLRMIKELDRLTACKPT 191
Db 805 PQBVKUQVQSQEELCMQVLLANTIPBLGRSQTOFEMRSYIREIKAQLRQKQWV 864

Oy 192 SCSSRFYQVLTKLUDSVQPIARELHQFTPDLIKSHMVSUDPEMMARLISVQPKLISGK 251
Db 865 SSQRFQFLQTLKUDNLHDLVQHQLYCLNTFPIOSRALSVEPFPMSEVIAQDPLKLAGM 924

Oy 252 VPKPYFH 258
Db 925 VKPLPFH 931

RESULT 7
US-08-764-870-15
Sequence 15, Application US/08764870
; Patent No. 6236946
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S
; APPLICANT: Baxter, John D
; APPLICANT: Flitterick, Robert J
; APPLICANT: Wagner, Richard L
; APPLICANT: Kushner, Peter J
; APPLICANT: Aprilletti, James W
; ADDRESS: Cooley Godward
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 93306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

RESULT 8
US-08-980-115-15
; Sequence 15, Application US/08980115
; Patent No. 6266622
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S
; APPLICANT: Baxter, John D
; APPLICANT: Flitterick, Robert J
; APPLICANT: Wagner, Richard L
; APPLICANT: Kushner, Peter J
; APPLICANT: Aprilletti, James W
; APPLICANT: West, Brian L
; APPLICANT: Shiu, Andrew K
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: UCAL-246/02US
; CURRENT APPLICATION NUMBER: US/08/980,115
; CURRENT FILING DATE: 1997-11-26

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (65) 0843-5000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-764-870-15

Query Match 48.5%; Score 665; DB 3; Length 984;
Best Local Similarity 52.9%; Pred. No. 2e-67; Mismatches 70; Indels 0; Gaps 0;
Matches 128; Conservative 44; Mismatches 70; Indels 0; Gaps 0;

Oy 17 VLAIRTPGVWAGHDNNOPDSFAALLSSNLNGEROLVHVVKWAKLPGFRNLHYDMA 76
Db 741 VLIENSPREVIVAGDSSKPAFDLNLSTLARLAKOMIQVWKVAKLPGKPNLPLDQT 800

Oy 77 VIQYSWGMMPAMGRSRFTNVNSRMLYFADLVNEYRMEKRSRMSQCVRMHSQBG 136
Db 801 LIQYSMCLLSPALSRYSKHTNSOFLXAFDVLVNEEKOMQSAMYZELCOCMHOISLQFV 860

Oy 137 WIQITPBLCKMALLSFILPVGLKRNKFPLBLRMIKELDRLTACKRKNPSCRR 196
Db 861 RIQLTFBETTMKVLLISTPDKLKSQAAPERNTRNKKERLQVTKPANSQSWQR 920

Oy 197 FYQVLTKLUDSVQPIARELHQFTPDLIKSHMVSUDPEMMARLISVQPKLISGK 256
Db 921 FYQVLTKLUDSVQPIARELHQFTPDLIKSHMVSUDPEMMARLISVQPKLISGK 980

Oy 257 FH 258
Db 981 FH 982

EARLIER APPLICATION NUMBER: 08/764,870
 EARLIER FILING DATE: 1996-12-13
 EARLIER APPLICATION NUMBER: 60/008,606
 EARLIER FILING DATE: 1995-12-14
 EARLIER APPLICATION NUMBER: 60/008,543
 EARLIER FILING DATE: 1995-12-13
 EARLIER APPLICATION NUMBER: 60/008,540
 EARLIER FILING DATE: 1995-12-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 984
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DOMAIN
 LOCATION: (695)..(969)
 OTHER INFORMATION: minimal ligand binding domain
 US-08-980-115-15

Query Match 48.5%; Score 665; DB 3; Length 984;
 Best Local Similarity 52.9%; Pred. No. 2e-67; Matches 128; Conservative 44; Mismatches 70; Indels 0; Gaps 0;
 Qy 17 VIEATEPGVUCAGHDNNQNPSEFAAISLNLGEGEROLVHVKWAGLPGRNPLRHDDQA 756
 Db 741 VLENTEPEPVIVAGYDGSKPTDAENLSTLNRLAKGKOMIOVUVKAWKYLPSFKNLPLEDIT 800
 Qy 77 VIQYSWMGLMVFFAMGRSFTVNNSRMLYFADLVNBYRMKRSYASOCURMHLUSOBERG 136
 Db 801 LIVYSMCLSLSPALSRSYKHTNSOLYRFLDVLVNEEKHQASANVLCQMHQSLSQV 860
 Qy 137 WLIQTRPQLCMKALIPLSIPVGDGLKNOKEPDLRNNTYKELDRITACKRKNPFCSCR 196
 Db 861 RLQLTPEBYTMKVLLISTPKDGKLSQAAPEMRNTYKELRKNTVKCPNNSQSWOR 920
 Qy 197 PYQTKLSDVOPARLHOFTDILKSHMWVDFPEMAEITIVQVPKILSGVKT 255
 Db 921 PYQTKLSDMSHDLVSDLSPCPYTFRESHALKVSPFAMLVETISDQLPKVSEGNAPLY 980
 Qy 257 PH 258
 Db 981 FH 982

RESULT 9
 ; Sequence 13, Application US/08764870
 ; GENERAL INFORMATION:
 : APPLICANT: Scanlan, Thomas S
 : APPLICANT: Baxter, John D
 : APPLICANT: Flatterick, Robert J
 : APPLICANT: Wagner, Richard L
 : APPLICANT: Kushner, Peter J
 : APPLICANT: Aprilletti, James W
 : APPLICANT: West, Brian
 : TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cooley Godward
 : STREET: Five Palo Alto Square, 3000 El Camino Real
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,870
 FILING DATE: 13-DEC-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,540
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,606
 FILING DATE: 13-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jackie N
 REGISTRATION NUMBER: 35,966
 REFERENCE/DOCKET NUMBER: UCAL-246/01US
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 777 amino acids
 TYPR: amino acid
 STRANDBNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-764-870-13

Query Match 49.3%; Score 662.5; DB 3; Length 777;
 Best Local Similarity 50.6%; Pred. No. 2.7e-67; Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;
 Qy 12 PIFANLRAIEPGVUCAGHDNNQNPSEFAAISLNLGEGEROLVHVKWAGLPGRNPLRHDDQA 71
 Db 530 PTIUSLVIKTEPEVLYAGWISSTPDSTWRIMTINLGGQVTAAVKVKALPGPRLHL 589
 Qy 72 DDONAVITOSWMGLMVFFAMGRSFTVNNSRMLYFADLVNBYRMKRSYASOCURMHLUSOBERG 131
 Db 590 DDQMTLQISWMPLMAFGWRSYROSSANLICFAPDILINBORMTLPCOMYDCKHMLV 649
 Qy 133 SQEGWTIQTQBLCMKALIPLSIPVGDGLKNOKEPDLRNNTYKELDRITACKRKNPFCSCR 191
 Db 650 SSELHLRLOVSYEBYLCKMUTLILSSVPKGKLSQBLFDEIRMYKELKGKAIYREGNS 709
 Qy 192 SCSPRFYQTKLSDVOPARLHOFTDILKSHMWVDFPEMAEITIVQVPKILSGVKT 251
 Db 710 QNNMPYQOTKLDMSHDLVSDLSPCPYTFRESHALKVSPFAMLVETISDQLPKVSEGNAPLY 980
 Qy 252 VKPYFHF 258
 Db 769 IKKULFH 775

RESULT 10
 ; Sequence 13, Application US/08980115
 ; GENERAL INFORMATION:
 : APPLICANT: Scanlan, Thomas S
 : APPLICANT: Baxter, John D
 : APPLICANT: Flatterick, Robert J
 : APPLICANT: Wagner, Richard L
 : APPLICANT: Kushner, Peter J
 : APPLICANT: Aprilletti, James W
 : APPLICANT: West, Brian L
 : APPLICANT: Shiu, Andrew K
 : TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
 : CURRENT APPLICATION NUMBER: US/08/980,115
 : CURRENT FILING DATE: 1997-11-26
 : EARLIER APPLICATION NUMBER: 08/764,870
 : EARLIER FILING DATE: 1996-12-13
 : EARLIER APPLICATION NUMBER: 60/008,606
 : EARLIER FILING DATE: 1995-12-14

EARLIER APPLICATION NUMBER: 60/008, 543
 EARLIER FILING DATE: 1995-12-13
 EARLIER APPLICATION NUMBER: 60/008, 540
 EARLIER FILING DATE: 1995-12-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 13
 LENGTH: 777
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DOMAIN
 LOCATION: (506)..(762)
 OTHER INFORMATION: minimal ligand binding domain
 US-08-980-115-13

Query Match 48.3%; Score 662.5; DB 3; Length 777;
 Best Local Similarity 50.6%; Pred. No. 27e-67;
 Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;
 Qy 12 PFLNVLRAIEPGVCAHGHDNQPDSTPAALLSSLINEGERQVHVKWAKALPGRNLHV 71
 Db 530 PTLVSLFVIREPVLYGSDSPVDPSTWRIMTLLNMGGRQTAATVKAALPGLPFNLHL 589

Qy 72 DDMAVIQSYWGMVAMGWASPTNVNSRMLYFADPVENETRMRHSRMSSOCVRMHL 131
 Db 590 DDQMTLQIYQSYWGMVAMGWASPTNVNSRMLYFADPVENETRMRHSRMSSOCVRMHL 649

Qy 132 SQRPGWQITPRPFLCKMALLFSITPVGKNGKEFDLNRNYKEDRTRACKRKNPT 191
 Db 650 SSELHQVQSYEYLCKMALLFSITPVGKNGKEFDLNRNYKEDRTRACKRKNPT 709

Qy 192 SCSRQYVOLTKLDSVQPIARSHQFTFDLKLHKSHMSVDFPERRMARIISVQPKLSGK 251
 Db 710 QMWQRYVQLTKLDSMHEVVENILNYCQTFDQTKM-SIEPEMLAKITINQPKVSGN 768

Qy 252 VPKVFA 258
 Db 769 IKKGJLFH 775

RESULT 11
 Sequence 8, Application US/08875223
 ; Parent No. 6127175
 ; GENERAL INFORMATION:
 ; APPLICANT: VIGNE, Emmanuelle
 ; APPLICANT: PERICAUDT, Michel
 ; APPLICANT: DEBIEU, Jean-Francois
 ; APPLICANT: ORSINI, Cecile
 ; APPLICANT: YEH, Patrice
 ; APPLICANT: LATTA, Martine
 ; APPLICANT: PROST, Edward
 TITLE OF INVENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT
 TITLE OF INVENTION: ADENOVIRUSES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEER: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, Mailstop 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875, 223
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PR 95/00747
 FILING DATE: 20-JAN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: FR 95/06532
 FILING DATE: 01-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: FR 95/10541
 FILING DATE: 08-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: FR WO FR96/00088
 FILING DATE: 19-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Fehner Esq., Paul F.
 REGISTRATION NUMBER: 35,135
 REFERENCE/DOCKET NUMBER: ST95005G1-US
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (610) 454-3808
 TOPOLGY: linear
 MOLECULE TYPE: protein
 US-08-875-223-8

Query Match 47.0%; Score 644.5; DB 3; Length 534;
 Best Local Similarity 51.3%; Pred. No. 1.8e-65;
 Matches 122; Conservative 46; Mismatches 69; Indels 1; Gaps 1;
 Qy 21 TEPGVYCAGHDNNQPDSPFALLSSLINEGERQVHVKWAKALPGRNLHVDDOMAVIQY 80
 Db 3 IPEPEVLYAG3DSSYFDPSTWRIMTLLNMGGRQTAIAVKWAKALPGRNLHVDDOMAVIQY 62

Qy 81 SWMGAVMVRGMWRFPTNVNSRMLYFADPVENETRMRHSRMSSOCVRMHLSSBFGWMQI 140
 Db 63 SWMFLMARAIGWSYROSSANLICFAPPDLTINFORMTLPOMYDQCKMILYVSSBLHLQY 122

Qy 141 TPQEFLCKMALLFSITPVGKNGKEFDLNRNYKEDRTRACKRKNPTCSRRFQL 200
 Db 123 SYEEFLCKMALLFSITPVGKNGKEFDLNRNYKEDRTRACKRKNPTCSRRFQL 182

Qy 201 TKLADSVQPIARESHQFTFDLKLHKSHMSVDFPERRMARIISVQPKLSGKVPDIYFH 258
 Db 183 TKLADSMEVVENILNYCQTFDQTKM-SIEPEMLAKITINQPKVSGNNGNIKKLFH 239

RESULT 12
 Sequence 2, Application US/09091042A
 ; Sequence 2, Application US/09091042A
 ; Parent No. 6455300
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America
 ; as represented by the Secretary/
 ; Department of Health and Human Services
 ; Washington, D.C.
 Htn Ph.D., Han
 Hager Ph.D., Gordon L.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING
 DNA BINDING MOLECULES IN LIVING CELLS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEER: Needle & Rosenberg
 STREET: 127 Peachtree Street, Suite 1200
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30333
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/091,042A

FILING DATE: 08-Jun-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/008,373

FILING DATE: 08-Dec-1995

ATTORNEY/AGENT INFORMATION:

NAME: Selby, Elizabeth

REGISTRATION NUMBER: 30298

REFERENCE/DOCKET NUMBER: 14014.0183

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 688-0770

TELEFAX: 404-688-9980

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 2;

US-09-091-042A-2

Query Match

Best Local Similarity 49.4%; Score 639.5; DB 4; Length 1070;

Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;

Qy 12 PFLNVLVLAIEPGVAGHNDNNOPDSFAALLSSNLGEROLVHVVWAKALPGPRLHV 71

Db 823 PTIVSLVLRVIRPEVLYAGSDSVDSPEDSAMVRIMTTANMGGRQTAAVKWAIGLNLHL 882

Qy 72 DDMQAVIQSYWMGLMFMAGMSFTNVNSRMLYFAPDIVERNTYRMHSRMTSOCVRARHL 131

Db 883 DDQMTLQYSWMLPMAFALGWSYRQSGNLICFADPLINFORMSLPGMVQDCKMLPV 942

Qy 132 SQRFGWILQITPOEFLCMKALLFSIIPVGDLKNOKEFDLBRMNYKELDRITACKRNPT 191

Db 943 SCLBQLQVSYEEVYLQMKTLLSSVPKGKSQFLPDEIRTYKELRAIKVREGSNS 1002

Qy 192 SCRRFTYQTLKLDSDVOPATARELHOFPTDPLIKSMVSDFPENNMAISVQVKLSK 251

Db 1003 QWWRFQLTKLDSMHEVVENLTYCFOTFLDKTM-SIEPPMLEAITNQIPKYSNGN 251

Qy 252 VPKIYFH 258

Db 1062 IKKLIFH 1068

RESULT 13

US-08-592-214A-24

Sequence 24, Application US/08592214A

Patent No. 5911536

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identity

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yanofsky, Martin F.

ADDRESS: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PC-DOS/ms-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,214

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,214A

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3291

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3297

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 284 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-592-214A-24

Query Match

Best Local Similarity 49.6%; Score 638.5; DB 2; Length 284;

Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;

Qy 12 PFLNVLVLAIEPGVAGHNDNNOPDSFAALLSSNLGEROLVHVVWAKALPGPRLHV 71

Db 97 DDQMTLQYSWMLPMAFALGWSYRQSGNLICFADPLINFORMSLPGMVQDCKMLPV 156

Qy 132 SQRFGWILQITPOEFLCMKALLFSIIPVGDLKNOKEFDLBRMNYKELDRITACKRNPT 191

Db 157 SSELBQLQVSYEEVYLQMKTLLSSVPKGKSQFLPDEIRTYKELRAIKVREGSNS 216

Qy 192 SCRRFTYQTLKLDSDVOPATARELHOFPTDPLIKSMVSDFPENNMAISVQVKLSK 251

Db 217 QWWRFQLTKLDSMHEVVENLTYCFOTFLDKTM-SIEPPMLEAITNQIPKYSNGN 275

Qy 252 VPKIYFH 258

Db 276 IKKLIFH 282

RESULT 14

US-09-149-976-24

Sequence 24, Application US/09149976

Patent No. 6127123

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identity

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/99/149,976

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,214

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 24:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 284 amino acids
 ;
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-09-149-976-24

Query Match Best Local Similarity 46.6%; Score 638.5; DB 3; Length 284; Matches 122; Conservative 49.4%; Pred. No. 3.5e-65; Mismatches 76; Indels 1; Gaps 1; Qy 12 PIFLNVLAIEPGVCAHGDNQPDSTAALLSNEIGEROLHVVKWAKALPGRFLHV 71 Db 37 PTVLSLVEVIREVLYAGDSSVPSA9RINTLNMGGRQVIAAKWAKILGLNLH 96 Qy 72 DDOMAVIQSYNGLVMGWRSPFTNNSRMLYAPDLPVENEYRMKRSRMSOCVRMHL 131 Db 97 DDQMTLQYSMMPLMAPALGWSYROSQSGNLCPADDLINEQRMSLPCMDCKMLFV 156 Qy 132 SQEFGMLOITPQBLCKMALLFSIIPVGIANKQKEDLMNYIKELDRACKRKNP 191 Db 157 SSELORLQSYEEYLCKMLLSSVPKEGLKSOELFDIRWTYIKELGKAIYREGNS 216 Qy 192 SCSCRFYQTLKLDSPQARELHQFTPELLIKHSWVDPEMAELSVQPKLGSK 251 Db 217 QNWQRFYQTLKLDSPMHEVUNLTYCQTEFLKTM-SIEPEMLABITNQPKYSGN 275 Qy 252 VPKIYFH 258 Db 276 IKKULFH 282

RESULT 15

US-07-716-827C-5
 ; Sequence 5, Application US/07716827C
 ; Patent No. 5215915
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Simons Jr., Stoney S.
 ; APPLICANT: Yamamoto, K. R.
 ; APPLICANT: Chakraborti, P. K.
 ; APPLICANT: Garabedian, M. J.
 ; TITLE OF INVENTION: SUPER GLUCOCORTICOID RECEPTORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cushman, Darby & Cushman
 ; STREET: Eleventh Floor, 1615 L Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036-5601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07-716,827C
 FILING DATE: 19910619
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Scott, Watson T.
 REGISTRATION NUMBER: 26,581
 REFERENCE DOCKET NUMBER: WTS/5683/84453
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)8613000
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:

; LENGTH: 795 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; US-07-716-827C-5

Query Match Best Local Similarity 46.6%; Score 638.5; DB 1; Length 795; Matches 122; Conservative 49.4%; Pred. No. 1.6e-64; Mismatches 76; Indels 1; Gaps 1; Qy 12 PIFLNVLAIEPGVCAHGDNQPDSTAALLSNEIGEROLHVVKWAKALPGRFLHV 71 Db 608 DDQMTLQYSMMPLMAPALGWSYROSQSGNLCPADDLINEQRMSLPCMDCKMLFV 667 Qy 132 SQEFGMLOITPQBLCKMALLFSIIPVGIANKQKEDLMNYIKELDRACKRKNP 191 Db 668 SSELORLQSYEEYLCKMLLSSVPKEGLKSOELFDIRWTYIKELGKAIYREGNS 727 Qy 192 SCSCRFYQTLKLDSPQARELHQFTPELLIKHSWVDPEMAELSVQPKLGSK 251 Db 728 QNWQRFYQTLKLDSPMHEVUNLTYCQTEFLKTM-SIEPEMLABITNQPKYSGN 786 Qy 252 VPKIYFH 258 Db 787 IKKULFH 793

Search completed: October 9, 2003, 11:42:40
 Job time : 20 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:38:28 ; Search time 45 Seconds

(without alignments)

917.087 Million cell updates/sec

Title: US-09-687-609A-1

Perfect score: 1371

Sequence: I-GSHMIEG3YECQPTFLNVEA.....SVOVPKLISGRKVPIYHTQ 260

Scoring table:

Gapext 10.0 , Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03;*

1: /SIDSL/geodata/geneseq/geneseq/geneseqp-emb1/AAI1980.DAT:*

2: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1981.DAT:*

3: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1982.DAT:*

4: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1983.DAT:*

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7: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1986.DAT:*

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9: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1988.DAT:*

10: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1989.DAT:*

11: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1990.DAT:*

12: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1991.DAT:*

13: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1992.DAT:*

14: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1993.DAT:*

15: /SIDSL/geodata/geneseq/geneseqp-emb1/AAI1994.DAT:*

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21: /SIDSL/geodata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDSL/geodata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDSL/geodata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIDSL/geodata/geneseq/geneseqp-emb1/AA2003.DAT:*

ALIGNMENTS

RESULT 1

ID AAB97073 standard; Protein; 260 AA.

XX AAB97073;

AC

XX

DT

31-JUL-2001 (first entry)

XX

DB

Rat androgen receptor ligand binding domain.

XX

Rat: androgen receptor; AR: ligand binding domain; LBD: osteopathic;

XX

crystallographic structure; AR-LBD; AR modulator; prostate cancer;

XX

age related disease; osteoporosis; muscle wasting; libido; vasotropin;

XX

protein coordinate data.

XX

OS Rattus sp.

XX

PN WO200127622-A1.

XX

PD

19-APR-2001.

XX

PF 13-OCT-2000; 2000W0-US28495.

XX

PR 14-OCT-1999; 99US-0159394.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Weismann R, Binegar H, Krystek SR, Sack JS, Salvati ME;

XX PI Tokarski JS, Wang C, Attar RM;

XX WPI; 2001-30022/31.

DR

Rat androgen recep

Rat androgen recep

Canine Androgen re

Human Androgen rec

Human androgen rec

Androgen receptor.

Human androgen rec

Breast cancer-assoc

Human androgen rec

Human androgen rec

Androgen-independe

Human androgen rec

Human androgen rec

Human androgen rec

Rat: androgen recep

Human steroid rece

Androgen receptor

Human androgen rec

TRP/ androgen rece

Human androgen rec

Amino acid sequenc

Ligand binding dom

Human progeserone

Chain A of structu

Geneswatch regulat

PT New crystallographic structure of the Androgen receptor ligand-binding domain, useful for identifying modulators of androgen receptors -
 XX
 PT
 XX
 PS Example; Page 27; 83pp; English.
 XX
 CC The present sequence is the rat androgen receptor (AR) ligand-binding domain (LBD). It is provided in an example illustrating an invention relating to a new crystallographic structure of the AR-LBD. The structure comprises either an AR-LBD and an AR-LBD ligand, or an AR-LBD without an AR-LBD ligand (where the crystal diffracts to at least 3 angstrom resolutions) and has a crystal stability within 5 % of its unit cell dimensions). The AR-LBD is useful for identifying modulators of the androgen receptor, which may be used for treating prostatic cancer and age related diseases such as osteoporosis, muscle wasting and loss of libido.

SQ Sequence 260 AA;

Query Match 100.0%; Score 1371; DB 22; Length 260;
 Best Local Similarity 100.0%; Pred. No. 3 8e-135; Mismatches 0; Indels 0; Gaps 0;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GSHMIEGTYCQPIFLNVLAEPVCAHGNQNQPSFAALISSNLIGEROLVHVKWA 60
 Db 1 GSHMIEGTYCQPIFLNVLAEPVCAHGNQNQPSFAALISSNLIGEROLVHVKWA 60

Oy 61 KALPGERMLHVDDOMAVIYQSMGLMFMAMGRSPFTNNSRMLYFADDLVNEYRMKSR 120
 Db 61 KALPGERMLHVDDOMAVIYQSMGLMFMAMGRSPFTNNSRMLYFADDLVNEYRMKSR 120

Oy 121 MISCOCVRARHLSLBFGWQITPQFLCMALLPSIPVDGLKNOKPFDLMNMYKELD 180
 Db 121 MISCOCVRARHLSLBFGWQITPQFLCMALLPSIPVDGLKNOKPFDLMNMYKELD 180

Oy 181 RIACKKNPTCSRRPYQLTKLDSVOPVIAERLHQFTFDLILKSHMVSDPEMMAEII 240
 Db 181 RIACKKNPTCSRRPYQLTKLDSVOPVIAERLHQFTFDLILKSHMVSDPEMMAEII 240

Oy 241 SVQVPKILSGKVKPIYHTQ 260
 Db 241 SVQVPKILSGKVKPIYHTQ 260

RESULT 2

ID ABB83821
 ID ABB83821 standard; Protein; 388 AA.
 AC ABB83821;
 XX DT 13-SEP-2002 (first entry)

DB Human androgen receptor variant AR42 SEQ ID NO 2.
 XX
 KW Human; androgen receptor; receptor; AR; AR42; AR32; tumour; cancer; steroid response element; prostate cancer; testis; gene therapy; hormone therapy; cytostatic; contraceptive.
 OS Homo sapiens.
 PN EP1213300-A1.

XX PD 12-JUN-2002.
 XX 26-OCT-2001; 2001EP-0250379.
 PR 30-NOV-2000; 2000EP-1061161.

PA (SCHD) SCHERING AG.
 XX PI Ahrens-Path T, Haendler B;
 XX DR WPI; 2002-550575/57.
 DR N-PSDB; ABN95656.

RESULT 3

AY21027
 ID AAY21627 standard; protein; 452 AA.
 AC AAY21627;
 XX DT 11-AUG-1999 (first entry)

DB Ligand binding domain of nuclear receptor hAr.
 XX KW Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glycerophosphate dehydrogenase; cardiac; obesity; triacyceride; plasma cholesterol; anti-hypertriacyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
 OS Homo sapiens.
 XX FN WO926966-A2.
 XX FD 03-JUN-1999.
 XX PP 25-NOV-1998; 98WO-US25296.

XX
PR 26-NOV-1997; 97US-0980115.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Apriletti JW, Baxter JD, Pletterick RJ, Kushner PJ;
PL Scanlan TS, Shlau AK, Wagner RL, West BL;
XX DR WPI; 1999-357810/30.
XX PT Modulating activity of a thyroid hormone receptor
PS Disclosure; FIG 3H-R; 447pp; English.
XX
CC The invention relates to a method for modulating activity of a thyroid
CC hormone receptor that comprises administration of an aromatic compound
CC which fits spatially and preferentially into a thyroid hormone ligand
CC binding domain. The aromatic compound (of a specified formula) can be
CC used to increase alpha-glycerophosphate (GDP) levels, at
CC levels which do not significantly modify cardiac GMP levels and are
CC indicated in the treatment of obesity. The compound also lower total
CC plasma cholesterol and triglyceride levels and can be used as anti-
CC hypertriglyceridemic-agents. The compound may also be used for treating
CC atherosclerosis and may be indicated in thyroid hormone replacement
CC therapy in patients with compromised cardiac function. Sequenced
CC amino acid sequences of ligand binding domains of several
CC members of the nuclear receptor superfamily.
XX SQ Sequence 452 AA;

Query Match 98.4%; Score 1349.5; DB 20; Length 452;
Best Local Similarity 99.6%; Pred. No. 1.5e-132; Mismatches 0; Indels 1; Gaps 1;
Matches 258; Conservative

QY 2 SHMIEGYECOPFLAVLNEIATRPGVCAHGNNQPDSPALISSLNEIGEROLVHVTWAK 61
Db 195 SH-IEGYECOPFLAVLNEIATRPGVCAHGNNQPDSPALISSLNEIGEROLVHVTWAK 253

QY 62 ALPGFRLNLHDQMAVIOQYSWGMGLMVAMGWMSFTNTNSRMLYFADLVNTEYRMKRM 121
Db 254 ALPGFRLNLHDQMAVIOQYSWGMGLMVAMGWMSFTNTNSRMLYFADLVNTEYRMKRM 313

QY 122 YSQCVRMRLHSOBFGWLOITPDRFLCKMALLFSITPVDGKKNOKPFDLMNYTKELDR 181
314 YSQCVRMRLHSOBFGWLOITPDRFLCKMALLFSITPVDGKKNOKPFDLMNYTKELDR 373

Db 182 IIACKRKNPPTCSRFRQLTKLDSVOPARRELQOPTPOLIKISMVSDFPEMMABIS 241
QY 374 IIACKRKNPPTCSRFRQLTKLDSVOPARRELQOPTPOLIKISMVSDFPEMMABIS 433

QY 242 VQVPKILSGKVVKPIYFHTQ 260
Db 434 VQVPKILSGKVVKPIYFHTQ 452

RESULT 4
ABG71292 ID ABG71292 standard; Protein; 839 AA.
XX AC ABG71292;
XX DT 08-JAN-2003 (first entry)
XX DB Human androgen receptor.

XX Pharmacological; receptor; endocrine disrupting chemical; EDC;
KW simultaneous determination; ligand binding activity; human;
KW androgen receptor.

XX Chimeric - Homo sapiens.
OS Chimeric - Bacteria.
OS Synthetic.

XX PN JP2002243739-A.
XX PT 28-AUG-2002.
XX PD 21-FEB-2001; 2001JP-0045420.
XX PR (TOYM) TOYBO KK.
XX PA WPI; 2002-744851/81.
DR N-PSDB; ABS56325.

XX PT A method and a kit for simultaneous determination of binding activity
PT of ligand with 2 or more receptors using their corresponding tracers -
XX PS Example 3; Page 13-15, 22pp; Japanese.

XX The present invention relates to a new method for simultaneous
CC determination of binding activity of a ligand with 2 or more receptors
CC using their corresponding tracers, and a kit for the determination.
The invention can be used for screening of ligands with pharmacological
CC activity via receptor and endocrine disrupting chemicals (EDCs). The
CC invention is advantageous as it allows simultaneous determination of
CC binding activity of ligand. The present amino acid sequence represents
CC the human androgen receptor as described in the invention.
XX SQ Sequence 839 AA;

Query Match 98.4%; Score 1349.5; DB 23; Length 839;
Best Local Similarity 99.6%; Pred. No. 3.6e-132; Mismatches 0; Indels 1; Gaps 1;
Matches 258; Conservative

Qy 2 SHMIEGYECOPFLAVLNEIATRPGVCAHGNNQPDSPALISSLNEIGEROLVHVTWAK 61
Db 582 SH-IEGYECOPFLAVLNEIATRPGVCAHGNNQPDSPALISSLNEIGEROLVHVTWAK 640

Qy 62 ALPGFRLNLHDQMAVIOQYSWGMGLMVAMGWMSFTNTNSRMLYFADLVNTEYRMKRM 121
Db 641 ALPGFRLNLHDQMAVIOQYSWGMGLMVAMGWMSFTNTNSRMLYFADLVNTEYRMKRM 700

Qy 122 YSQCVRMRLHSOBFGWLOITPDRFLCKMALLFSITPVDGKKNOKPFDLMNYTKELDR 181
Db 701 YSQCVRMRLHSOBFGWLOITPDRFLCKMALLFSITPVDGKKNOKPFDLMNYTKELDR 760

Qy 182 IIACKRKNPPTCSRFRQLTKLDSVOPARRELQOPTPOLIKISMVSDFPEMMABIS 241
Db 761 IIACKRKNPPTCSRFRQLTKLDSVOPARRELQOPTPOLIKISMVSDFPEMMABIS 820

Qy 242 VQVPKILSGKVVKPIYFHTQ 260
Db 821 VQVPKILSGKVVKPIYFHTQ 839

RESULT 5
AAG68238 ID AAG68238 standard; Protein; 839 AA.
XX AC AAG68238;
XX DT 08-FEB-2002 (first entry)
XX DB Fused androgen receptor (AR) protein SEQ ID NO:11.
XX Human; androgen receptor; AR; fused androgen receptor protein;
KW fusion androgen receptor protein; sugar-combining protein;
KW maltose-combining protein.
XX Chimeric - Homo sapiens.
OS Chimeric - Unidentified.
XX PN JP2001252080-A.
XX

PD 18-SEP-2001.
 XX
 PR 13-MAR-2000; 2000JP-0069030.
 XX
 PR 13-MAR-2000; 2000JP-0069030.
 XX
 PA (TOYOMI) TOYOB0 KK.
 XX
 DR WPI; 2002-029658/04.
 XX
 DR N-PSDB; ABA01683.
 XX
 PT New polypeptide for screening drugs, comprises an androgen receptor protein fused with a sugar-combining protein -
 XX
 PS Claim 8; Page 11-13; 16pp; Japanese.
 XX
 CC The present invention describes a fused androgen receptor protein with a sugar-combining protein prepared by fusing an androgen receptor protein with the above fused AR protein. Also described are: (1) a gene encoding the above fused AR protein; (2) a vector carrying the above gene; (3) a transformant in which the above vector is introduced to a microbe and a gene encoding the fused AR protein is expressed; (4) the preparation of a fused AR protein in which the above transformant is cultured and the fused AR protein is collected from the resultant culture; and (5) a reagent for detecting the presence of interaction with a ligand containing the above fused AR protein, a solvent for dissolving chemical substances and a diluent liquid of the dissolved chemical substances. The fusion protein can be used for screening drugs. The present sequence represents the AR protein and sugar-combining protein fusion protein from the present invention.
 XX
 SQ Sequence 839 AA;
 Query Match 98.4%; Score 1349.5; DB 23; Length 839;
 Best Local Similarity 99.6%; Pred. No. 3.9e-132; Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 CC
 Oy 2 SHMIEGYECQIFLNLVLEIPGVVCAAGHDNNQPSFAALLSSNELGEROLVHVKWAK 61
 Db 592 SH-IEGYECQIFLNLVLEIPGVVCAAGHDNNQPSFAALLSSNELGEROLVHVKWAK 640
 Oy 62 ALPGFRNLHVDDOMAVIQSWMGLAVFANGWRSFTNVNSRMLYFAPDLYENYRMKSRM 121
 Db 641 ALPGFRNLHVDDOMAVIQSWMGLAVFANGWRSFTNVNSRMLYFAPDLYENYRMKSRM 700
 Oy 122 YSOCVRMHLSQFGWLQITPQBLCLMALLSIIIPDGKNOKEFELRMNYYKELDR 181
 Db 701 YSOCVRMHLSQFGWLQITPQBLCLMALLSIIIPDGKNOKEFELRMNYYKELDR 760
 Oy 182 IIACKRKNPCTSCSRRTYQITKLDSVQIPARBLHOFTDLIKSHMSVDPPEMMATIS 241
 Db 761 IIACKRKNPCTSCSRRTYQITKLDSVQIPARBLHOFTDLIKSHMSVDPPEMMATIS 820
 Oy 242 VQPKILSGKVKPYIYHTQ 260
 Db 821 VQPKILSGKVKPYIYHTQ 839
 RESULT 6
 AAE32995 ID AAE32995 standard; Protein; 895 AA.
 XX
 AC AAE32995;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Macaca mulatta androgen receptor (rhAR).
 XX
 KW Androgen receptor; rhAR protein; bone formation; atherosclerosis; acne;
 KW myoanabolism; sarcopenia; benign prostatic hyperplasia; hypogonadism;
 KW lipid metabolism; hirsutism; prostate disease; hippocampal function;
 KW cancer; rhesus monkey; single nucleotide polymorphism; SNP; therapy.
 XX
 OS Macaca mulatta.
 XX
 PH Location/Qualifiers
 PT Misc-difference 210
 PT /note= "This residue changes to Gly due to single nucleotide polymorphism (SNP)"
 PT Domain 535...600
 PT /note= "DNA binding domain"
 XX
 PR WO200290529-A1.
 XX
 PD 14-NOV-2002.
 XX
 PR 03-MAY-2002; 2002WO-US14175.
 XX
 PR 08-MAY-2001; 2001US-289573P.
 XX
 PA (MERI) MERCK & CO INC.
 PI Towler DA, Chen F;
 DR WPI; 2003-103516/09.
 DR N-PSDB; AAD50740.
 XX
 PT New DNA encoding Macaca mulatta androgen receptor (rhAR) protein, useful for screening rhAR agonists and/or antagonists, and in identifying tissue selective androgen compounds such as those active in bone formation or myoanabolism -
 PT bone formation or myoanabolism -
 XX
 PS Claim 25; Page 38; 84pp; English.
 XX
 CC The invention relates to a DNA encoding Macaca mulatta androgen receptor (rhAR) protein. Nucleic acid molecules of the invention are useful for screening agonists and/or antagonists of rhAR and in identifying tissue selective androgen compounds including those active in bone formation, myoanabolism, treatment of sarcopenia, benign prostatic hyperplasia, acne, hirsutism, male hypogonadism, atherosclerosis, relief of post-menopausal symptoms, treatment and prevention of prostate or breast cancer and management of lipids. AR modulators may be used to regulate development, production and maintenance of bone and muscle, in the treatment of prostate disease and in regulation of lipid metabolism and hippocampal function. The present sequence is Macaca mulatta (rhesus monkey) androgen receptor.
 XX
 SQ Sequence 895 AA;
 Query Match 98.4%; Score 1349.5; DB 24; Length 895;
 Best Local Similarity 99.6%; Pred. No. 3.9e-132; Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 CC
 Oy 2 SHMIEGYECQIFLNLVLEIPGVVCAAGHDNNQPSFAALLSSNELGEROLVHVKWAK 61
 Db 638 SH-IEGYECQIFLNLVLEIPGVVCAAGHDNNQPSFAALLSSNELGEROLVHVKWAK 696
 Oy 62 ALPGFRNLHVDDOMAVIQSWMGLAVFANGWRSFTNVNSRMLYFAPDLYENYRMKSRM 121
 Db 697 ALPGFRNLHVDDOMAVIQSWMGLAVFANGWRSFTNVNSRMLYFAPDLYENYRMKSRM 756
 Oy 122 YSOCVRMHLSQFGWLQITPQBLCLMALLSIIIPDGKNOKEFELRMNYYKELDR 181
 Db 757 YSOCVRMHLSQFGWLQITPQBLCLMALLSIIIPDGKNOKEFELRMNYYKELDR 816
 Oy 182 IIACKRKNPCTSCSRRTYQITKLDSVQIPARBLHOFTDLIKSHMSVDPPEMMATIS 241
 Db 817 IIACKRKNPCTSCSRRTYQITKLDSVQIPARBLHOFTDLIKSHMSVDPPEMMATIS 876
 Oy 242 VQPKILSGKVKPYIYHTQ 260
 Db 877 VQPKILSGKVKPYIYHTQ 895
 RESULT 7
 AAE32996

ID	AAB32996	standard; Protein; 895 AA.	Db	757 YSQCVTRKHLISQSRGMLQITPQLCKRALKLPSIPVDCIKNQKFDPDRBMYVIKELDR	816
XX			QY	182 IACKRKPTCSRRLFQVLTKLDSVQPAERLHOTPDPLIKSHMSVPDPEMMARIS	241
AC	AAB32996;		DB	817 IIACKRKPTCSRRLFQVLTKLDSVQPAERLHOTPDPLIKSHMSVPDPEMMARIS	876
DT	02-APR-2003	(first entry)	OY	242 VQVKILSGKPKIVHTQ	260
XX			DB	877 VQVKILSGKPKIVHTQ	895
DB	Macaca mulatta androgen receptor (rhAR) allelic variant protein.				
XX	Androgen receptor; rhAR protein; bone formation; atherosclerosis; acne; myoanabolism; barcpenia; benign prostatic hyperplasia; hypogonadism; lipid metabolism; hirsutism; prostate disease; hippocampal function; cancer; rhesus monkey; single nucleotide polymorphism; SNP; therapy.				
XX	Macaca mulatta.				
OS					
XX					
PY	Key' location/Qualifiers				
FT	misc-difference 210	/note= "wild-type Glu is changed to Gly due to single nucleotide polymorphism (SNP)" 535:600 /note= "DNA binding domain"			
FT	Domain				
FT					
XX					
PN	W020030529-A1.				
XX					
PD	14-NOV-2002.				
XX					
PP	03-MAY-2002; 2002WO-US14175.				
XX					
PR	08-MAY-2001; 2001US-289573P.				
XX					
PA	(MERI) MERICK & CO INC.				
XX					
PI	Towler DA, Chen F;				
XX					
DR	WPI; 2003-103516/09.				
DR	N-PSDB; AAB50741.				
XX					
PT	New DNA encoding Macaca mulatta androgen receptor (rhAR) protein, useful for screening rhAR agonists and/or antagonists, and in identifying tissue selective androgen compounds such as those active in bone formation or myoanabolism				
PT					
PT	Claim 55; Page 46; 89pp; English.				
CC	The invention relates to a DNA encoding Macaca mulatta androgen receptor (rhAR) protein. Nucleic acid molecules of the invention are useful for screening agonists and/or antagonists of rhAR and in identifying tissue selective androgen compounds including those active in bone formation, myoanabolism, treatment of sarcopenia, benign prostatic hyperplasia, acne, hirsutism, male hypogonadism, atherosclerosis, relief of post-menopausal symptoms, treatment and prevention of prostate or breast cancer and management of lipids. AR modulators may be used to regulate development, production and maintenance of bone and muscle, in the treatment of prostate disease and in regulation of lipid metabolism and hippocampal function. The present sequence is Macaca mulatta (rhesus monkey) androgen receptor allelic variant protein.				
XX					
PS	Sequence 895 AA;				
XX					
PT	Query Match Best Local Similarity 99.4%; Score 1349.5; DB 24; Length 895; Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
QY	2 SHIMIGSYCQPIFLNVLRAIEPGWVCAHGHDNNQPSAALLSINELGEROIVHVTWK 61				
DB	638 SH-IEGYECQPIFLNVLRAIEPGWVCAHGHDNNQPSAALLSINELGEROIVHVTWK 696				
OY	62 ALPGFRMLHVDDOMAVIQYSWGMVQITPQBLCKRALKLPSITPVDGKNGKEDELRNYTKELDR 121				
DB	697 ALPGFRMLHVDDOMAVIQYSWGMVQITPQBLCKRALKLPSITPVDGKNGKEDELRNYTKELDR 756				
OY	122 YSQCVVRKHLISQSRGMLQITPQLCKRALKLPSIPVDCIKNQKFDPDRBMYVIKELDR 181				
XX					
Query Match	98.4%; Score 1349.5; DB 24; Length 895;				

Best Local Similarity 99.6%; Pred. No. 4e-132; 0; Mismatches 1; Indels 1; Gaps 1;

Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query 2 SHIMIREGYRCQPIPLVLAIRPGWVCAHGHNQDPSFALLSINELGEROLVHVKWAK 61
 Database 642 SH-IRGYECQPIPLVLAIRPGWVCAHGHNQDPSFALLSINELGEROLVHVKWAK 703

Qy 62 ALPGFRNLHVDDOMAVIYQSMGLMVFAMGRSFIVNSRMLYFAPDVENYRMKSRM 61
 Db 701 ALPGFRNLHVDDOMAVIYQSMGLMVFAMGRSFIVNSRMLYFAPDVENYRMKSRM 700

Qy 122 YSQCVRMRLHSOBFGNLIQTPQBLCMKALLSIIIPVDGLKNOQKFDELRYMYIKELDR 181
 Db 761 YSQCVRMRLHSOBFGNLIQTPQBLCMKALLSIIIPVDGLKNOQKFDELRYMYIKELDR 181

Qy 182 IACKRKNTPSCSRPFYQLTKLDSVOPATARELHOPTFDLILKSHMVSDFPMMARIS 241
 Db 821 IACKRKNTPSCSRPFYQLTKLDSVOPATARELHOPTFDLILKSHMVSDFPMMARIS 880

Qy 242 VQVPKILSGKVKPIYHTQ 260
 Db 881 VQVPKILSGKVKPIYHTQ 899

RESULT 9

ID AAP93110 AAP93110 standard; protein; 902 AA.

XX AC AAP93110; 25-MAR-2003 (updated)

AC DT 19-MAR-1990 (first entry)

DE Rat androgen receptor.

KW Rat androgen receptor; monoclonal antibody; polyclonal antibody; cancer.

KX OS Rattus rattus.

XX PN WO8909791-A; PR 14-APR-1988; PA (UYNC-) UNTV OF N CAROLINA.

XX PT 13-APR-1989; DR XX; PA (UYNC-) UNTV OF N CAROLINA.

XX PT WO8909791-A; DR WO8909791-A; PA (UYNC-) UNTV OF N CAROLINA.

XX PT French PS, Wilson EM, Joseph DR, Lubahn DB; DR WO; 1989-324206/44.

XX PT DNA encoding androgen receptor protein - useful for transforming eukaryotic hosts for protein expression and subsequent antibody prodn. Disclosure, Fig. 5; 41pp; English.

CC Androgen receptor protein (AR) is used to produce mono- or poly-clonal antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating prostate cancers to determine responsiveness to androgen withdrawal therapy. (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 902 AA;

Query Match 98.4%; Score 1349.5; DB 10; Length 902; Best Local Similarity 99.6%; Pred. No. 4e-132; Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 SHIMIREGYRCQPIPLVLAIRPGWVCAHGHNQDPSFALLSINELGEROLVHVKWAK 61
 Db 645 SH-IRGYECQPIPLVLAIRPGWVCAHGHNQDPSFALLSINELGEROLVHVKWAK 703

Qy 62 ALPGFRNLHVDDOMAVIYQSMGLMVFAMGRSFIVNSRMLYFAPDVENYRMKSRM 121
 Db 704 ALPGFRNLHVDDOMAVIYQSMGLMVFAMGRSFIVNSRMLYFAPDVENYRMKSRM 763

Qy 122 YSQCVRMRLHSOBFGNLIQTPQBLCMKALLSIIIPVDGLKNOQKFDELRYMYIKELDR 181
 Db 764 YSQCVRMRLHSOBFGNLIQTPQBLCMKALLSIIIPVDGLKNOQKFDELRYMYIKELDR 823

Qy 182 IACKRKNTPSCSRPFYQLTKLDSVOPATARELHOPTFDLILKSHMVSDFPMMARIS 241
 Db 824 IACKRKNTPSCSRPFYQLTKLDSVOPATARELHOPTFDLILKSHMVSDFPMMARIS 883

Qy 242 VQVPKILSGKVKPIYHTQ 260
 Db 884 VQVPKILSGKVKPIYHTQ 902

RESULT 10

ID AAP91006 AAP91006 standard; protein; 902 AA.

XX AC AAP91006; 25-MAR-2003 (updated)

DT 28-FEB-1990 (first entry)

DB Rat androgen receptor DNA clone.

XX KW Androgen receptor; TR2 polypeptide;

XX OS Rat.

XX PT Key Location/Qualifiers

FT Region 1..902

FT /*tag= a /product=98 kd polypeptide

FT Region 170..902

FT /*tag= b /product=79 kd polypeptide

XX PT WO8909223-A.

XX PT WO8909223-A.

XX PD 05-OCT-1989.

XX PT 24-MAR-1989; 89WO-JP01238.

XX PR 30-MAR-1988; 88US-0176107.

PR 05-OCT-1988; 88US-0252807.

PR 21-FEB-1989; 89US-0312763.

XX PA (ARCH-) ARCH DEV CORP.

XX PI Liao S, Chang C;

XX DR WPI: 1989-309501/42.

XX PI N-PSDB; AN91578.

XX PT New DNA encoding new androgen receptor and TR2 polypeptide(s) - able to bind DNA, and derived antibodies, useful for receptor assay and purification.

XX PS Claim 8; Fig 3; 60pp; English.

XX CC The protein is used to raise antibodies for receptor assays and for affinity purification.

CC The 98 kd product starts at the first Met codon; the 79 kd product starts from the second.

CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 902 AA;

Query Match 98.4%; Score 1349.5; DB 10; Length 902;
 Best Local Similarity 99.6%; Pred. No. 4e-132; Mismatches 0; Indels 1; Gaps 1;
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 2 SHMIEGYPECQIFNLYVLAIEPGVWCAHGDNQPSPAFLISLNELGEROLVHVKWAK 61
 DB 645 SH-IEGYECQPIFLNVLEAIEPGVWCAHGDNQPSPAFLISLNELGEROLVHVKWAK 703

OY 62 ALPGFRNLHVDDOMAVIQYSGMLVPMGWRSPFTVNSRMVYAPDLYENYRMKRM 121
 DB 704 ALPGFRNLHVDDOMAVIQYSGMLVPMGWRSPFTVNSRMVYAPDLYENYRMKRM 763

OY 122 YSQCVRMRLHSQERGMQLQTPOEFLCMKALLFSTIPDGSKNOKFDELRMNYKELDR 181
 DB 764 YSQCVRMRLHSQERGMQLQTPOEFLCMKALLFSTIPDGSKNOKFDELRMNYKELDR 823

OY 182 IIACKRKNPSCSRRPYQVOTKLDSVOPARBLHOFTEFLIKSHMVSDFPEMAELIS 241
 DB 824 IIACKRKNPSCSRRPYQVOTKLDSVOPARBLHOFTEFLIKSHMVSDFPEMAELIS 883

DB 884 VQVPKILSGKVPKIVFHTQ 902

RESULT 11

ABGT4229
 ID ABG74229 standard; Protein: 907 AA.
 XX
 AC ABG74229;
 DT 16-APR-2003 (first entry)
 #X DB Canine Androgen receptor.

XX Dog; receptor; androgen receptor; AR; cyrostatic; osteopathic;
 KW neuroleptic; canine disorder; cancer; mood disorder; temper disorder;
 KW frailty; muscular degeneration; bone loss.

OS Canis familiaris.
 XX US2002161194-A1.
 PN
 PD 31-OCT-2002.

XX 09-NOV-2001; 2001US-0008739.
 PP
 PR 09-NOV-2000; 2000US-247373P.

PA (CAST/) CASTLEBERRY T A.
 PA (LUBB/) LU B.
 PA (OWEN/) OWEN T A.
 PA (SMOC/) SMOCK S L.

PI Castleberry TA, Lu B, Owen TA, Smock SL;
 DR WPI; 2003-209230/20.
 XX N-PSDB; ABX16536.

PT New isolated canine androgen receptor protein, useful for diagnosing, classifying, prognosis and/or treating canine diseases (e.g. cancer) and in studying the molecular and biochemical actions of androgens in canine bone.

PT The invention relates to an isolated proteinaceous molecule having canine androgen receptor (AR) activity (appearing as ABGT4229), optionally

Query Match 98.4%; Score 1349.5; DB 24; Length 907;
 Best Local Similarity 99.6%; Pred. No. 4e-132; Mismatches 0; Indels 1; Gaps 1;
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 2 SHMIEGYPECQIFNLYVLAIEPGVWCAHGDNQPSPAFLISLNELGEROLVHVKWAK 61
 DB 650 SH-IEGYECQPIFLNVLEAIEPGVWCAHGDNQPSPAFLISLNELGEROLVHVKWAK 708

OY 62 ALPGFRNLHVDDOMAVIQYSGMLVPMGWRSPFTVNSRMVYAPDLYENYRMKRM 121
 DB 709 ALPGFRNLHVDDOMAVIQYSGMLVPMGWRSPFTVNSRMVYAPDLYENYRMKRM 768

OY 122 YSQCVRMRLHSQERGMQLQTPOEFLCMKALLFSTIPDGSKNOKFDELRMNYKELDR 181
 DB 769 YSQCVRMRLHSQERGMQLQTPOEFLCMKALLFSTIPDGSKNOKFDELRMNYKELDR 828

OY 182 IIACKRKNPSCSRRPYQVOTKLDSVOPARBLHOFTEFLIKSHMVSDFPEMAELIS 241
 DB 829 IIACKRKNPSCSRRPYQVOTKLDSVOPARBLHOFTEFLIKSHMVSDFPEMAELIS 888

DB 889 VQVPKILSGKVPKIVFHTQ 907

RESULT 12

AY33491
 ID AY33491 standard; Protein: 918 AA.
 XX
 AC AY33491;
 XX
 DT 19-JAN-2000 (first entry)
 XX Human androgen receptor protein.

XX Prosopoptotic; dependence domain; p75NTR; androgen receptor; DCC; huntingtin polyptide; Machado-Joseph disease; SCA1; SC12; SC16; Alzheimer's disease; Kennedy's disease; spinocerebellar atrophy; stroke; dentatorubropallidoluysian atrophy; cell proliferation; cell survival; neoplastic; malignant; autoimmune; fibrotic.

XX Homo sapiens.

XX WO945944-A1.
 XX
 PD 16-SEP-1999.
 XX
 PP 11-MAR-1999; 99WO-US05250.
 XX

PR	12-MAR-1998;	98US-0041886.	PT	Region	1..919
XX	(BURN-) BURNHAM INST.		PT	/wt% a	/wt% a
PA			PT	/product=98 kd polypeptide	/product=98 kd polypeptide
XX			PT	185..919	185..919
PI	Bredesen DE, Rabizadeh S;		PT	/*tag# b	/*tag# b
XX			PT	/product=79 kd polypeptide	/product=79 kd polypeptide
DR	WPI; 1989-561617/47.		XX		
XX	N-PSDB; AAZ23424.		PN	W08909223-A.	
PT	New proapoptotic dependence peptides, used to develop products for		XX		
PT	treating, e.g., Alzheimer's disease -		PD	05-OCT-1989.	
XX			XX	24-MAR-1989;	89WO-JP01238.
PS	Disclosure; Page 90-93; 1989P; English.		XX		
CC	This invention describes novel pure proapoptotic dependence peptides which comprise a sequence of an active dependence domain selected from		PR	30-MAR-1988;	88US-0176107.
CC	dependence polypeptides consisting of P75NTR, androgen receptor, DCC,		PR	05-OCT-1988;	88US-0253807.
CC	Huntington polypeptide, Machado-Joseph disease gene product, SCA1, SCA2,		PR	21-FEB-1989;	88US-0312763.
CC	SCM6 and atrophin-1 polypeptide. The proapoptotic peptides are capable		PA	(ARCH-) ARCH DEV CORP.	
CC	of inducing cell death and can be used to develop products to mediate or		XX		
CC	inhibit apoptosis. The methods can be used for reducing the severity of		PI	Liao S, Chang C;	
CC	a proapoptotic dependence domain mediated pathological conditions e.g.		XX		
CC	Huntington's disease, Alzheimer's disease, Kennedy's disease,		DR	WPI; 1989-309501/42.	
CC	Machado-Joseph disease, dentatorubro-pallidoluysian atrophy,		XX	N-PSDB; AN91577.	
CC	Spirocerabellar ataxias, dentatorubro-pallidoluysian atrophy,		PT	New DNA encoding new androgen receptor and TR2 polypeptide(s) - able	
CC	reducing the severity of a pathological condition mediated by upregulated		PT	to bind DNA, and derived antibodies, useful for receptor assay and	
CC	cell proliferation or cell survival e.g. neoplastic, malignant, or		XX	purification.	
CC	autoimmune or fibrotic conditions. This sequence represents a human		PS	Claim 8; FIG 3; 60PP; English.	
XX	androgen receptor described in the method of the invention.		XX		
SQ	Sequence 918 AA;		CC	The protein is used to raise antibodies for receptor assays and for	
	Query Match 98.4%; Score 1349.5; DB 20; Length 918;		CC	affinity purification.	
	Best Local Similarity 99.6%; Pred. No. 4.1e-132; Mismatches 0; Indels 1; Gaps 1;		CC	The 98 kd product starts at the first Met codon;	
	Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		CC	Starts from the second.	
			CC	(Updated on 25-MAR-2003 to correct PR field.)	
RY	2 SHIMIREGYCOPIFNLVLEAERGVVAGHDDNNQPSDFALLSSLINEGERQLVHVVKWAK 61		CC	(Updated on 25-MAR-2003 to correct PA field.)	
Db	661 SH-IEGYECQPIFLVLEAERGVVAGHDDNNQPSDFALLSSLINEGERQLVHVVKWAK 719		XX	Sequence 919 AA;	
QY	62 ALPGFRNLHVDDOMAVIQLQYSWNGLAFAMGRSFPTNNSRMYFAPDLYNEYRHMKSRM 121		CC	Query Match 98.4%; Score 1349.5; DB 10; Length 919;	
Db	720 ALPGFRNLHVDDOMAVIQLQYSWNGLAFAMGRSFPTNNSRMYFAPDLYNEYRHMKSRM 779		CC	Best Local Similarity 99.6%; Pred. No. 4.1e-132; Mismatches 0; Indels 1; Gaps 1;	
QY	122 YSQCVRMRHLISQPFGLMQLITPOFLCKMALLFSIIPVGGLKQKFDELRYNKYIKELDR 181		CC	Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
Db	780 YSQCVRMRHLISQPFGLMQLITPOFLCKMALLFSIIPVGGLKQKFDELRYNKYIKELDR 839		CC	Sh-IEGYECQPIFLVLEAERGVVAGHDDNNQPSDFALLSSLINEGERQLVHVVKWAK 720	
QY	182 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 241		QY	62 ALPGFRNLHVDDOMAVIQLQYSWNGLAFAMGRSFPTNNSRMYFAPDLYNEYRHMKSRM 121	
Db	840 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 899		Db	721 ALPGFRNLHVDDOMAVIQLQYSWNGLAFAMGRSFPTNNSRMYFAPDLYNEYRHMKSRM 780	
QY	242 VQVPKILSGKVKPITYHTQ 260		QY	122 YSQCVRMRHLISQPFGLMQLITPOFLCKMALLFSIIPVGGLKQKFDELRYNKYIKELDR 181	
Db	900 VQVPKILSGKVKPITYHTQ 918		Db	781 YSQCVRMRHLISQPFGLMQLITPOFLCKMALLFSIIPVGGLKQKFDELRYNKYIKELDR 840	
RESULT 13			QY	182 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 241	
AA90996			Db	841 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 900	
ID	AAP0996 standard; protein; 919 AA.		QY	242 VQVPKILSGKVKPITYHTQ 260	
XX			Db	901 VQVPKILSGKVKPITYHTQ 919	
AC	AAP0996;		RESULT 14		
DT	25-MAR-2003 (updated)		AAW14783	182 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 241	
DT	28-FEB-1990 (first entry)		AAW14783	841 IIACKRKNPFTCSRPFYQLTKLUDSVQPIARELHQFTFDLILTKSHMVSVDPEMMAEIIS 900	
DE	Human androgen receptor DNA clone.		AC	242 VQVPKILSGKVKPITYHTQ 260	
XX			AAW14783;	901 VQVPKILSGKVKPITYHTQ 919	
KW	Androgen receptor; TR2 polypeptide;		DT	22-JUN-1997 (first entry)	
OS	Homo sapiens.		XX		
XX					
Key	Location/Qualifiers				
FH					

DE Audrogen receptor.
 XX
 KW Androgen receptor; acidic fibroblast growth factor; aFGF;
 KW antisense; benign prostatic hyperplasia; prostate cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9711170-A1.
 XX
 PD 27-MAR-1997.
 XX
 PR 20-SEP-1996; 96WO-US15081.
 PR 20-SEP-1995; 95US-0004018.
 PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.
 PT Zamecnik PA;
 XX
 DR WPI; 1997-202879/18.
 DR N-FSDB; AAT63407.
 XX
 PT Oligonucleotide(s) antisense to human androgen receptor and acidic
 PT FGF genes - used to inhibit gene expression, for the treatment of
 PT benign prostatic hyperplasia.
 XX
 PS Disclosure; Page 22-28; 51PP; English.
 XX
 CC Human androgen receptor (AAW14733) binds testoaterone and, acting
 at the transcriptional level, regulates the growth of normal
 CC prostatic cells. Antisense oligonucleotides (see also AR63100,
 CC AT63404-05) based on an androgen receptor cDNA clone (see also
 CC AR63407) can be used to prevent androgen receptor gene expression,
 CC thereby inhibiting the growth or survival of prostatic cells for
 CC the treatment of benign prostatic hyperplasia and prostate cancer.
 XX
 SQ Sequence 919 AA;
 Query Match 98.4%; Score 1349.5; DB 18; Length 919;
 Best Local Similarity 99.6%; Pred. No. 4.1e-132;
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 2 SHMISGEGBCOPFLAVNLFAIRPEGVCAHGNQDPSFAALLSSNLEGEROLVHVKWAK 61
 Db 662 SH-IEGYRCOPFLAVNLFAIRPEGVCAHGNQDPSFAALLSSNLEGEROLVHVKWAK 720
 Qy 62 ALPGFRNLHYDDOMAVIYQSMGLMFAMGNGSPINTNSRMYFAPDLYVNEYRHKSRM 121
 Db 721 ALPGFRNLHYDDOMAVIYQSMGLMFAMGNGSPINTNSRMYFAPDLYVNEYRHKSRM 780
 Qy 122 YSQCVRMRLHSQEPGMQLQTPOBFLCMKALLFSIIPVQGLKNOKEFDLRYMYKELDR 181
 Db 781 YSQCVRMRLHSQEPGMQLQTPOBFLCMKALLFSIIPVQGLKNOKEFDLRYMYKELDR 840
 Qy 182 IIACKRKNPSCSRRFKLTKLDSVOPARIHLHQFFPDLIKSHMVSDFPENNMAIS 241
 Db 841 IIACKRKNPSCSRRFKLTKLDSVOPARIHLHQFFPDLIKSHMVSDFPENNMAIS 900
 Qy 242 VQVPKILSGKVPIYHTQ 240
 Db 901 VQVPKILSGKVPIYHTQ 919
 RESULT 15
 AAY78914
 ID AAY78914 standard; protein; 919 AA.
 XX AAY78914;
 AC AAY78914;
 DT 23-MAY-2000 (first entry)
 XX Human androgen receptor (AR) amino acid sequence.

KW Androgen receptor; AR; androgen-independent activation; inhibitor;
 KW cancer; benign prostatic hyperplasia; hirsutism; androgenic alopecia;
 KW acne; breast cancer; Kennedy disease; prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200001813-A2.
 XX
 PD 13-JAN-2000.
 XX
 PR 30-JUN-1999; 99WO-CA00504.
 PR 30-JUN-1998; 98US-0091871.
 PA (UYBR-) UNTV BRITISH COLUMBIA.
 PT Sadar ND, Bruchovsky N, Gout PW, Snoek R, Mawji NR;
 XX
 DR WPI; 2000-182113/16.
 XX
 PT Novel non-androgen ligand binding peptides for inhibiting
 PT androgen-independent activation of androgen receptor, used for
 PT screening compounds and for treatment of androgen-mediated diseases
 PT such as prostate cancer -
 XX
 PS Disclosure; Page 7; 32PP; English.
 XX
 CC This sequence represents the human androgen receptor (AR) amino acid
 CC sequence. The invention relates to a fragment of the AR corresponding to
 CC amino acids 234-391 (see AAY8913). The fragment mediates
 CC androgen-independent activation of the AR. The androgen receptor acts as
 CC a transcription factor, regulating the expression of certain
 CC androgen-responsive genes. Interaction of the AR with the protein kinase
 CC signal transduction pathway involves interaction with the androgen
 CC independent region. The AR fragment and peptides derived from it can be
 CC used as agents for inhibiting androgen independent activation of the
 CC androgen receptor, as activation domain, and as a tool for screening
 CC for compounds which affect androgen-independent activation of the AR.
 CC The peptides, when used in combination with androgen deprivation,
 CC effectively limit androgen mediated disease progression. These diseases
 CC include cancer, benign prostatic hyperplasia, hirsutism, androgenic
 CC alopecia, acne, breast cancer, Kennedy disease, and especially prostate
 CC cancer. The peptides and nucleic acids encoding them, are especially used
 CC for the treatment of androgen-mediated diseases, especially prostate
 tumours in patients deprived of androgen.
 XX
 SQ Sequence 919 AA;
 Query Match 98.4%; Score 1349.5; DB 21; length 919;
 Best Local Similarity 99.6%; Pred. No. 4.1e-132;
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 2 SHMISGEGBCOPFLAVNLFAIRPEGVCAHGNQDPSFAALLSSNLEGEROLVHVKWAK 61
 Db 662 SH-IEGYRCOPFLAVNLFAIRPEGVCAHGNQDPSFAALLSSNLEGEROLVHVKWAK 720
 Qy 62 ALPGFRNLHYDDOMAVIYQSMGLMFAMGNGSPINTNSRMYFAPDLYVNEYRHKSRM 121
 Db 721 ALPGFRNLHYDDOMAVIYQSMGLMFAMGNGSPINTNSRMYFAPDLYVNEYRHKSRM 780
 Qy 122 YSQCVRMRLHSQEPGMQLQTPOBFLCMKALLFSIIPVQGLKNOKEFDLRYMYKELDR 181
 Db 781 YSQCVRMRLHSQEPGMQLQTPOBFLCMKALLFSIIPVQGLKNOKEFDLRYMYKELDR 840
 Qy 182 IIACKRKNPSCSRRFKLTKLDSVOPARIHLHQFFPDLIKSHMVSDFPENNMAIS 241
 Db 841 IIACKRKNPSCSRRFKLTKLDSVOPARIHLHQFFPDLIKSHMVSDFPENNMAIS 900
 Qy 242 VQVPKILSGKVPIYHTQ 260
 Db 901 VQVPKILSGKVPIYHTQ 919

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